

GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 24, 2006, 20:19:49 ; Search time 7101 Seconds
(without alignments)

10860.525 Million cell updates/sec

Title: US-10-031-902A-36

Perfect score: 1206
Sequence: 1 gfgccctcagcttcaagt.....aaataaaccataactac 1206

Scoring table: IDENTITY_NUC
Gapex 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

GenBdb1:*
1: gb_env:*
2: gb_pat:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
7: gb_rts:*
8: gb_sy:*
9: gb_un:*
10: gb_vl:*
11: gb_ov:*
12: gb_hlg:*
13: gb_in:*
14: gb_cm:*
15: gb_da:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1206	100.0	1206	6	AF321553 Mus muscu
2	1200.4	99.5	1235	6	AY320031 Mus muscu
3	855	70.9	870	6	BC106776 Mus muscu
4	684	56.7	684	6	AF350409 Mus muscu
5	669.4	55.5	862	6	AY137338 Mus muscu
6	667.8	55.4	4263	6	AF320599 Mus muscu
7	667.8	55.4	197971	6	AC142191 Mus muscu
8	667.8	55.4	210200	6	AC157659 Mus muscu
9	629.2	52.2	2232	2	CQ086866 Sequence
10	624.4	51.8	984	6	AY137342 Mus muscu
11	624.4	51.8	1096	6	AY137341 Mus muscu
12	602	49.9	988	6	AF121352 Mus muscu
13	602	49.9	1014	6	AY137345 Mus muscu
14	601.8	49.9	933	6	AY256576 Mus muscu
15	601.4	49.9	1016	6	AY256575 Mus muscu
16	601.4	49.9	1026	6	AY137344 Mus muscu
17	601.4	49.9	1093	6	AY256574 Mus muscu
18	497.4	41.2	598	6	AB091386 Mus muscu

19	452.4	37.5	693	6	AF350411	AF350411 Mus muscu
20	364.4	30.2	1628	6	AF321552	AF321552 Rattus no
21	336.4	27.9	2127	6	BC051091	BC051091 Mus muscu
22	335.2	27.8	1464	6	BC086997	BC086997 Rattus no
23	318.4	26.4	1490	6	BC021766	BC021766 Mus muscu
24	316.6	26.3	797	6	AF350410	AF350410 Mus muscu
25	254.8	21.1	2714	6	AF320595	AF320595 Mus muscu
26	254.8	21.1	4679	6	AY137339	AY137339 Mus muscu
27	254.8	21.1	75164	2	CQ086895	CQ086895 Sequence
28	254.8	21.1	193034	6	AC174446	AC174446 Mus muscu
29	254.8	21.1	208074	12	AC153989	AC153989 Mus muscu
30	254.8	21.1	209064	6	AC159305	AC159305 Mus muscu
31	249.6	20.7	191955	6	AC102693	AC102693 Mus muscu
32	249.6	20.7	208074	12	AC153989	AC153989 Mus muscu
33	233.6	19.4	835	5	AY084051	AY084051 Homo sapi
34	213	17.7	9546	6	AY137343	AY137343 Mus muscu
35	204.4	16.9	62919	12	AC099883	AC099883 Mus muscu
36	179.2	14.9	230611	12	AC126655	AC126655 Rattus no
37	176	14.6	250	2	BD223286	BD223286 Toxicolog
38	169	14.0	16817	6	AC132352	AC132352 Mus muscu
39	169	14.0	231239	12	AC133164	AC133164 Mus muscu
40	167.4	13.9	9450	6	AF320596	AF320596 Mus muscu
41	167.4	13.9	303656	12	AC025528	AC025528 Mus muscu
42	145	12.0	166259	10	AY689436	AY689436 Deerpox v
43	143.8	11.9	823	5	AF285087	AF285087 Homo sapi
44	143.8	11.9	843	2	CQ727163	CQ727163 Sequence
45	143.8	11.9	850	2	CS034009	CS034009 Sequence

ALIGNMENTS

RESULT 1
AF321553
LOCUS
DEFINITION Mus musculus osteoclast inhibitory lectin (Oc11) mRNA, complete

AF321553 1206 bp mRNA linear ROD 07-MAY-2001
AF321553
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
Mus musculus

REFERENCE
AUTHORS Zhou,H., Kartsoiannis,V., Hu,Y.S., Elliott,J., Quinn,J.M.,
McKinstry,W.J., Gillespie,M.T. and Ng,K.W.,
A novel osteoblast-derived C-type lectin that inhibits osteoclast
formation
1 (bases 1 to 1206)

TITLE
JOURNAL J. Biol. Chem. 276 (18), 14916-14923 (2001)

REFERENCE
PUBMED 11278931
2 (bases 1 to 1206)

TITLE
JOURNAL Direct Submission
Submitted (15-NOV-2000) Department of Medicine, St. Vincent's
Hospital, The University of Melbourne, 41 Victoria Parade, Fitzroy,
Victoria 3065, Australia
location/Qualifiers

FEATURES
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CDS
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 PQAFATCMOEAQOLARFDNODLPLMRYNAPDSWITGHRSESEHMKMTDNTREYNT
 IPIRGERPBYLINNGIISIRIYSLMMWICSLKINYSIHCQIPFPFS"

Query Match 100.0%; Score 1206; DB 6; Length 1206;
 Best Local Similarity 100.0%; Pred. No. 1, Le-292;
 Matches 1206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGCTCTGAGCTTTCAAGTTTCAATCTGTAGTGGAAAACAGCTCTTCAAGCTTGAAGA 60
 DB 1 GTGGCTCTGAGCTTTCAAGTTTCAATCTGTAGTGGAAAACAGCTCTTCAAGCTTGAAGA 60
 QY 61 TGTGTGTCAAAAAGGCTTCCCTACCTATGCTTATGCCACAGGACCCGAGAGAGTGG 120
 DB 61 TGTGTGTCAAAAAGGCTTCCCTACCTATGCTTATGCCACAGGACCCGAGAGAGTGG 120
 QY 121 AAGTGGGTAAATTTCTCAAGAAAAGGACGGAACCAATCTCCCTGAGTCTTGTGCTA 180
 DB 121 AAGTGGGTAAATTTCTCAAGAAAAGGACGGAACCAATCTCCCTGAGTCTTGTGCTA 180
 QY 181 AGCTTACTGCTATATGAGATGATCATGGTCTCTCACTGAGCTGTAATGCTCTTCTG 240
 DB 181 AGCTTACTGCTATATGAGATGATCATGGTCTCTCACTGAGCTGTAATGCTCTTCTG 240
 QY 241 TGTGCTTGTGCAAGAAAAGACAGACAGATCCCACTGCAACAGACCTAATGCTGCTGGC 300
 DB 241 TGTGCTTGTGCAAGAAAAGACAGACAGATCCCACTGCAACAGACCTAATGCTGCTGGC 300
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 DB 301 CCCAAACTGGAATTTGGAATTAATGTTTTATTTTCTGAAATCCCAAGTAAC 360
 QY 361 GGAATCTGCGCCAGGCTCTTGTGATGACAGAGGCCCACTAGCTGGTGGTGAACAC 420
 DB 361 GGAATCTGCGCCAGGCTCTTGTGATGACAGAGGCCCACTAGCTGGTGGTGAACAC 420
 QY 421 AGGATAGCTGAATTTCTTAATAGATACAAAGCGCAATTTGTAATCTGATGGCTGCG 480
 DB 421 AGGATAGCTGAATTTCTTAATAGATACAAAGCGCAATTTGTAATCTGATGGCTGCG 480
 QY 481 ACAGAGAGTGTGAGAGCAACCTTGGAAAGTGAACAGACCACTGAGTATTAACAACGA 540
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 DB 601 GGATCTATTCACCTTGGATGTGATCTGTAGCAAGCTCAACAGCTATAGCTCCACAGCC 660
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 DB 661 AAACCTCTTTTTCCTTCTAGCATTTTACCAAGAGAGCTTTTAAAGCTTTATCTGTG 720
 QY 721 GGTGTACTCTTTCCTTATGATGATCCCAAGTGTATCAAAACAGATAGAGAAATTTCTT 780
 DB 721 GGTGTACTCTTTCCTTATGATGATCCCAAGTGTATCAAAACAGATAGAGAAATTTCTT 780
 QY 781 AACATGAGAAATGAAAAACCATCATTTTCAATTCATGAGAGAAATGTTAGGTAAATATC 840
 DB 781 AACATGAGAAATGAAAAACCATCATTTTCAATTCATGAGAGAAATGTTAGGTAAATATC 840
 QY 841 ACTGACTACTCTTCCGAGAGTCTGAGTTCACATCTGAGAACACATGCTGCTCAAA 900
 DB 841 ACTGACTACTCTTCCGAGAGTCTGAGTTCACATCTGAGAACACATGCTGCTCAAA 900
 QY 901 ACATCCGTAATGAGATCTTCTGAGGTATGAAAAACGCTACACTGTACTTTATCTGTG 960
 DB 901 ACATCCGTAATGAGATCTTCTGAGGTATGAAAAACGCTACACTGTACTTTATCTGTG 960

QY 961 CAATTTAAAGCATGAGGAGCATATGAGAGTATGCTACCCACATGATAGTCCCAAAA 1020
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 DB 1021 GGAAGAAATTAACAGGCTAAAGAAAGCTCTTGAACCTTTTCATCTTTCTTCCCTCTTG 1080
 QY 1081 GTCTTTTAAACCAAGTCTGCTGAGAGAAAGACATGAGAAATGCGGGAAGGAGG 1140
 DB 1081 GTCTTTTAAACCAAGTCTGCTGAGAGAAAGACATGAGAAATGCGGGAAGGAGG 1140
 QY 1141 GAGAGGACATGATTGGGGAGGAGGAGGAGGAAATTAATTAATAAAATTAACCAAA 1200
 DB 1141 GAGAGGACATGATTGGGGAGGAGGAGGAGGAAATTAATTAATAAAATTAACCAAA 1200
 QY 1201 TACTAC 1206
 DB 1201 TACTAC 1206

RESULT 2
 AY320031 1235 bp mRNA linear ROD 10-MAR-2004
 LOCUS
 DEFINITION
 Mus musculus osteoclast inhibitory lectin (Oc1l) mRNA, complete cds.
 ACCESSION
 AY320031
 VERSION
 AY320031.1 GI:33356564
 KEYWORDS
 SOURCE
 ORGANISM
 Mus musculus (house mouse)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Murioidea; Muridae; Murinae; Mus.
 REFERENCE
 AUTHORS
 Carlyle,J.R., Jamieson,A.M., Gasser,S., Clingan,C.S., Arase,H. and Raulot,D.H.
 Missing self-recognition of Oc1l/Clr-b by inhibitory NKR-P1 natural killer cell receptors
 Proc. Natl. Acad. Sci. U.S.A. 101 (10), 3527-3532 (2004)
 PUBMED
 14990792
 JOURNAL
 2 (bases 1 to 1235)
 AUTHORS
 Carlyle,J.R., Jamieson,A.M., Gasser,S., Clingan,C.S., Arase,H. and Raulot,D.H.
 Direct Submission
 Submitted (10-0UN-2003) Molecular & Cell Biology, University of California Berkeley, 485 Life Sciences Addition #3200, Berkeley, CA 94720-3200, USA

TITLE
 JOURNAL
 FEATURES
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 /protein_id="AA016529.1"
 /db_xref="GI:33356565"
 /translation="MCTVKASIPMLSPGSPQEVVEVGILOGRKHGTISPESCAKLYC"

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OM nucleic - nucleic search, using sw model

Run on: May 24, 2006, 20:19:57 ; Search time 5491 Seconds
(Without alignments)
12281.682 Million cell updates/sec

Title: US-10-031-902A-36

Perfect score: 1206

Sequence: 1 gggccctcagcttcaagf.....aaataaaccataactac 1206

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_est7:*
7: gb_est8:*
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10: gb_est11:*
11: gb_est12:*
12: gb_est13:*
13: gb_est14:*
14: gb_est15:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	627.6	52.0	2232	6	AK014570	AK014570 Mus muscu
2	627.6	52.0	2403	6	AK137753	AK137753 Mus muscu
3	602	49.9	2764	6	AK041724	AK041724 Mus muscu
4	502	41.6	969	4	BY714008	BY714008 BY714008
5	449.4	37.3	477	7	BF454103	BF454103 maasb09.
6	446.4	37.0	468	7	AM113425	AM113425 MC1988 mo
7	439.8	36.5	468	4	CB581560	CB581560 AGNNTC:N
8	432.4	35.9	444	7	BF660971	BF660971 ma71b03.
9	431.4	35.8	444	1	AI180635	AI180635 uc67f09.t
10	424	35.2	444	1	BF453698	BF453698 ma71b03.
11	421.2	34.9	448	7	AM113424	AM113424 MC1998 mo
12	407.8	33.8	926	7	BF182123	BF182123 601804663
13	394	32.7	394	2	BG091810	BG091810 mac17g04.
14	391.8	32.5	399	1	AA177493	AA177493 mt15c09.t
15	372	30.8	658	4	BY723071	BY723071 BY723071
16	370	30.7	394	1	AA797274	AA797274 wa23e07.t
17	365.8	30.3	401	2	BG230151	BG230151 mac28d03.
18	365	30.3	376	1	AA218025	AA218025 mv59f08.t
19	362	30.0	362	7	BF146984	BF146984 uw72b04.y

20	358	29.7	391	1	AA797334	AA797334 wa23g07.t
21	348.4	28.9	352	7	AW987086	AW987086 ut13h04.x
22	338	28.0	338	1	AI786472	AI786472 ut13h04.y
23	336.4	27.9	894	3	BU523257	BU523257 AGNCCOURT
24	318.4	26.4	2158	6	AK090364	AK090364 Mus muscu
25	310.4	25.7	560	3	BQ264893	BQ264893 NISC ff02
26	309.8	25.7	976	3	BQ935069	BQ935069 AGNCCOURT
27	308	25.5	1212	6	AK017207	AK017207 Mus muscu
28	304.4	25.2	317	1	AA472200	AA472200 v998e12.x
29	298.2	24.7	688	4	BY733654	BY733654 U1-R-BJ2-
30	285	23.6	285	2	BG095407	BG095407 mac28d03.
31	278.6	23.1	848	10	DV728509	DV728509 RYL21153
32	275.4	22.8	304	1	AA172733	AA172733 mt06c10.t
33	273	22.6	673	4	BY716938	BY716938 BY716938
34	258.2	21.4	858	4	CA468141	CA468141 AGNCCOURT
35	254.6	21.1	508	1	AI641897	AI641897 vq47h05.y
36	251	20.8	534	1	AI504668	AI504668 vq33d10.x
37	248.2	20.6	691	5	CK843446	CK843446 ut1-R-BJ2-
38	239.2	19.8	926	2	BF783690	BF783690 602109488
39	236.4	19.6	428	1	AA871981	AA871981 vq47h05.t
40	233.2	19.3	572	4	BX520363	BX520363 BX520363
41	232.6	19.3	853	7	AM107057	AM107057 ul192d06.y
42	223.2	18.5	503	7	BF407755	BF407755 U1-R-BJ2-
43	216.2	17.9	509	1	AI230483	AI230483 EST227178
44	216.2	17.9	531	4	CB718857	CB718857 AKGNNC:U
45	211.8	17.6	699	10	DV227774	DV227774 EST-AR161

ALIGNMENTS

LOCUS	AK014570	2232 bp	mRNA	linear	HTC 02-SEP-2005
DEFINITION	Mus musculus 0 day neonate skin cDNA, RIKEN full-length enriched library, clone:632413B12 product:c LECTIN-RELATED PROTEIN C homolog [Mus musculus], full insert sequence.				
ACCESSION	AK014570				
VERSION	AK014570.1	GI:12852505			
KEYWORDS	HTC; CAP trapper.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidae; Muridae; Murinae; Mus.				
AUTHORS	Carninci, P. and Hayashizaki, Y.				
TITLE	High-efficiency full-length cDNA cloning				
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)				
PUBMED	10349636				
REFERENCE					
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Query Match 52.0%; Score 627.6; DB 6; Length 2232;

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JOURNAL      Nature 409, 685-690 (2001)
REFERENCE    The FANTOM Consortium, the RIKEN Genome Exploration Research Group
AUTHORS     Phase I and II Team.
TITLE       Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
JOURNAL      Nature 420, 563-573 (2002)
REFERENCE    RIKEN Genome Exploration Research Group, Genome Science Group
AUTHORS     (Genome Network Core Team) and the FANTOM Consortium.
TITLE       Antisense transcription in the Mammalian Transcriptome
JOURNAL      Science 309, 1564-1566 (2005)
REFERENCE    The PANTOM Consortium, Riken Genome Exploration Research Group and
AUTHORS     Genome Science Group (Genome Network Project Core Group).
TITLE       The Transcriptional Landscape of the Mammalian Genome
JOURNAL      Science 309, 1559-1563 (2005)
REFERENCE    Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H.,
AUTHORS     Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukushima, T.,
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            Tejima, Y., Toyra, T., Yamamura, T., Yasunishi, A., Yoshida, K.,
            Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
TITLE       Direct Submission
JOURNAL      Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
REFERENCE    Physical and Chemical Research (RIKEN), Laboratory for Genome
AUTHORS     Exploration and Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa, 230-0045, Japan (E-mail: genome-res@sc.riken.jp,
            URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT      cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.jp/.
            URL:http://fantom.gsc.riken.jp/.
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[illegible]

GenCore version 5.1.8
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Run on: May 24, 2006, 20:45:02 ; Search time 269 Seconds
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8388.689 Million cell updates/sec

Title: US-10-031-902A-36

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 93554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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3	102	8.5	519	US-09-531-056A-3	Sequence 3, Appl1
4	102	8.5	582	US-09-531-056A-1	Sequence 1, Appl1
5	102	8.5	931	US-09-531-056A-9	Sequence 9, Appl1
6	93.4	7.7	90050	US-09-245-041-5	Sequence 5, Appl1
7	93.4	7.7	90050	US-09-358-055B-5	Sequence 5, Appl1
8	93.4	7.7	90050	US-09-893-238-5	Sequence 5, Appl1
9	92.8	7.7	44576	US-09-484-629B-17	Sequence 17, Appl1
10	86.4	7.2	90050	US-09-245-041-5	Sequence 5, Appl1
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13	85.6	7.1	7874	US-09-780-175-96	Sequence 17, Appl1
14	85.6	7.0	48974	US-08-920-422-17	Sequence 17, Appl1
15	84.4	7.0	14707	US-09-312-762A-3	Sequence 3, Appl1
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17	83.6	6.9	44576	US-09-484-629B-17	Sequence 17, Appl1
18	81.6	6.8	13011	US-08-791-849A-14	Sequence 14, Appl1
19	81.6	6.8	17056	US-09-245-041-3	Sequence 3, Appl1
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22	81.4	6.7	9196	US-09-971-773-3	Sequence 3, Appl1
23	80.2	6.7	1652	US-10-199-945A-28	Sequence 28, Appl1

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C 26	78.2	6.5	3205	3	US-09-061-768A-3	Sequence 3, Appl1
C 27	78.2	6.5	3205	3	US-09-764-246-3	Sequence 3, Appl1
C 28	77.4	6.4	1259	3	US-09-809-545A-40	Sequence 40, Appl1
C 29	76.2	6.3	1422	3	US-09-784-642-6	Sequence 6, Appl1
C 30	76.2	6.3	48974	3	US-08-920-422-17	Sequence 17, Appl1
C 31	76	6.3	14507	3	US-08-785-150-1	Sequence 1, Appl1
C 32	76	6.3	14507	3	US-09-660-299-1	Sequence 1, Appl1
C 33	76	6.3	14507	3	US-09-435-377-1	Sequence 1, Appl1
C 34	76	6.3	14507	3	US-09-973-928-1	Sequence 1, Appl1
C 35	75.8	6.3	2801	3	US-09-869-588-27	Sequence 27, Appl1
C 36	75.6	6.3	600	7	PCT-US93-10418-1	Sequence 1, Appl1
C 37	75.6	6.3	1662	3	US-09-023-655-1241	Sequence 1, Appl1
C 38	75.6	6.3	1676	3	US-09-949-016-4428	Sequence 4428, Ap
C 39	75.6	6.3	1702	3	US-09-023-655-1391	Sequence 1391, Ap
C 40	74.6	6.2	37950	3	US-09-949-016-258	Sequence 258, App
C 41	74.6	6.2	37950	3	US-09-338-907-183	Sequence 183, App
C 42	74.6	6.2	37950	3	US-09-218-207-183	Sequence 183, App
C 43	74.2	6.2	5039	3	US-09-386-816C-1	Sequence 1, Appl1
C 44	74.2	6.2	5039	3	US-10-320-176-1	Sequence 1, Appl1
C 45	73.4	6.1	35828	3	US-09-449-218D-17	Sequence 17, Appl1

ALIGNMENTS

RESULT 1
US-09-949-016-4429
Sequence 4429, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTRI, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C1001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4429
LENGTH: 843
TYPE: DNA
ORGANISM: Human
US-09-949-016-4429

Query Match 11.9%; Score 143.8; DB 3; Length 843;
Best Local Similarity 62.7%; Pred. No. 2.6e-35;
Matches 259; Conservative 0; Mismatches 147; Indels 7; Gaps 2;

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Db 578 TCTAGATTTACGACAAAGCCCACTAATCTTTAGAGCATATTGGAAGTGA 630

RESULT 2

US-09-531-056A-5
; Sequence 5, Application US/09531056A
; Patent No. 6455683
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: DNA MOLECULES ENCODING HUMAN CLAX PROTEINS AND THEIR SOLUBLE FUSI
; FILE REFERENCE: DB20 NP
; CURRENT APPLICATION NUMBER: US/09/531,056A
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 5
; LENGTH: 573
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-531-056A-5

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QY 349 ACCCAAGTAACTGACATTTGCCAGGCTTTCGATGAGCAAGAGGCCCACTAGCTC 408
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QY 469 GGATGGCTGCAAGAGTGTCTCAAGCACCTTGGAGTGGACAGACAACTAGT 528
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; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: DNA MOLECULES ENCODING HUMAN CLAX PROTEINS AND THEIR SOLUBLE FUSI
; FILE REFERENCE: DB20 NP
; CURRENT APPLICATION NUMBER: US/09/531,056A
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin version 3.0

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; ORGANISM: Homo sapiens
US-09-531-056A-3

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; Patent No. 6455683
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; TITLE OF INVENTION: DNA MOLECULES ENCODING HUMAN CLAX PROTEINS AND THEIR SOLUBLE FUSI
; FILE REFERENCE: DB20 NP
; CURRENT APPLICATION NUMBER: US/09/531,056A
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 1
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US-09-531-056A-1

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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3	159.8	13.3	429	9 US-09-960-352-14614	Sequence 14614, A
4	144.4	12.0	1560	6 US-10-114-893-21	Sequence 21, Appl
5	144	11.9	2536	9 US-10-719-993-136	Sequence 136, App
6	144	11.9	2542	9 US-10-719-993-131	Sequence 131, App
7	144	11.9	2595	9 US-10-719-993-133	Sequence 133, App
8	144	11.9	2595	9 US-10-719-993-132	Sequence 132, App
9	144	11.9	2628	9 US-10-719-993-135	Sequence 135, App
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11	143.8	11.9	850	7 US-10-770-639-5	Sequence 5, Appl
12	143.8	11.9	850	12 US-10-501-841-28	Sequence 28, Appl
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17	143.8	11.9	2595	9 US-10-388-838-31	Sequence 31, Appl

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23	102.6	8.5	2238	6	US-10-114-893-27	Sequence 27, Appl	
24	102.2	8.5	2706	9	US-10-719-993-130	Sequence 130, App	
25	102.2	8.5	2710	9	US-10-719-993-137	Sequence 137, App	
26	102	8.5	897	3	US-09-965-529-45	Sequence 45, Appl	
27	102	8.5	897	3	US-09-969-680A-45	Sequence 45, Appl	
28	102	8.5	897	13	US-11-048-692-45	Sequence 45, Appl	
29	102	8.5	1091	10	US-10-450-763-19609	Sequence 19609, A	
30	102	8.5	2706	9	US-10-388-838-15	Sequence 15, Appl	
31	102	8.5	2710	9	US-10-388-838-25	Sequence 25, Appl	
c	32	101.6	8.4	42514	6	US-10-087-192-475	Sequence 475, App
c	33	101.2	8.4	92969	11	US-10-330-773-178	Sequence 178, App
34	100	8.3	454	8	US-10-242-535A-43386	Sequence 43386, A	
35	100	8.3	454	8	US-10-085-783A-43386	Sequence 43386, A	
36	99.6	8.3	23611	8	US-10-322-281-61	Sequence 61, Appl	
c	37	98.6	8.2	50833	11	US-10-330-773-188	Sequence 188, App
c	38	98.6	8.2	59767	10	US-10-461-862-157	Sequence 157, App
c	39	97.8	8.1	236246	11	US-10-330-773-567	Sequence 567, App
40	97.6	8.1	78953	7	US-10-085-117-31	Sequence 31, Appl	
c	41	97.2	8.1	22281	6	US-10-087-192-91	Sequence 1155, Ap
42	96.6	8.0	35159	6	US-10-087-192-91	Sequence 91, Appl	
43	96.2	8.0	5315	8	US-10-451-867A-1	Sequence 1, Appl	
c	44	94.6	7.8	107432	11	US-10-330-773-137	Sequence 137, App
45	94.2	7.8	38239	11	US-10-330-773-603	Sequence 603, App	

ALIGNMENTS

RESULT 1									
US-10-388-838-12									
; Sequence 12, Application US/10388838									
; Publication No. US20040180344A1									
; GENERAL INFORMATION:									
; APPLICANT: David W. Morris									
; TITLE OF INVENTION: Novel Therapeutic Targets in Cancer									
; FILE REFERENCE: 529452001600									
; CURRENT APPLICATION NUMBER: US/10/388,838									
; NUMBER OF SEQ ID NOS: 114									
; SOFTWARE: FastSeq for Windows Version 4.0									
; SEQ ID NO 12									
; LENGTH: 2232									
; TYPE: DNA									
; ORGANISM: Mus musculus									
US-10-388-838-12									
Query Match									
Best Local Similarity 52.2%; Score 629.2; DB 9; Length 2232;									
Matches 736; Conservative 0; Mismatches 78; Indels 20; Gaps 4;									
QY	128	TAAATTCCTCCAGGAAAAAGCAGCGAACATCTCCCTGAGTCTTGCTAAGCTTTA	187						
DB	295	TAAATTCCTCCAGGAAAAAGCTCAGAGCACTCCCTGAGTCTTGCTAAGCTTTA	354						
QY	188	CTGCTACTATGAGTGTATCATGTGCTCTCACTGTAGCTGTATATGCTCTTCTTGCTTT	247						
DB	355	CTGCTCTATGAGTGTATCATGTGCTCTCACTGTAGCTGTATATGCTCTTCTTGCTTT	414						
QY	248	GTCAGCAACAAACAGACAGATCCAGTCCAGCAACAGACTTATGCTGCTCCGCAAAA	307						
DB	415	GTCAGTACAAACAGACAGATCTTATATCAACAAAGCTTATGCTGCTCCGCAAAA	474						
QY	308	CTGATGTGAGTGAATTAATATGTTTTTATTTTCTGAATACCAAGTACGACATT	367						
DB	475	CTGATGTGAGTGAATTAATATGTTTTTATTTTCTGAATACCAAGTACGACATT	534						
QY	368	CGCCAGGCGCTTGTGATGCGACAAAGGCGCCAACTAGCTCGGTTTGACAAACAGATGA	427						

Db 535 TGCCAGACCTTCTGATGGCAAGAGGCCAAGCTAGCTGGTTTGAACAAGAGAGGA 594
Qy 428 GCTGAATTTCTTAATAGATATCAAGGCAATTTTGAATCTCTGATTTGGCTGACAGAA 487
Db 595 GCTGAATTTCTTAATAGATATCAAGGCAATTTTGAATCTCTGATTTGGCTGACAGAA 654
Qy 488 GTGCTAGAGCAACCTTGGAGTGAAGAGCAACACCTGATTAACAACAGATTTCCAT 547
Db 655 GTGCTAGAGCAACCTTGGAGTGAAGAGCAACACCTGATTAACAACAGATTTCCAT 714
Qy 548 CCGGGAGAGGAAAGATTTGCTTACTGAAACAACGCGATCAGACATGACAGATCTA 607
Db 715 CAGAGGAGTGAACATGTGCTTACTGAGCGGCAATGGGATCAGAGATTCAGGACAT 774
Qy 608 TTCACTTGGAGTGAATCTGTAGCAAGCTCAACAGCTATAGCTTCCATCCAACTCC 667
Db 775 TATACCTCGAATATGATCTGTAGCAAGCTTAAACAATAGCTTCCAACTCC 834
Qy 668 TTTTCTTCTCTTCTAGCATTTTACCAAGAGACGCTTTTGAAGCTTATCTGTGGTCTA 727
Db 835 ---TGTTCTGCTTACGATTTTACCAAGAGACCTTCTAGCTTATCTATGGTGTCTA 891
Qy 728 CTCTTTCCTTATGATGCCAAGAGTCTATCAACAGATAGAGATATTTCTTAACATCA 787
Db 892 CTTTTCCTTATGATGCCAAGAGTCTATCAACAGGATTTGAATATTTTAAAGCTCG 951
Qy 788 GAATGAAACCTCTCATTTTCTTATGACAGAGATTTGTAGTGTAAATCACTGACT 847
Db 952 CAATGAAACCTCTCAAGGCTCTTGAAGATTTGCTTCCGTATGTTAAGA-GACTGACT 1004
Qy 848 ACTCTTCCGAAGTCTGATGATCACTGAGCAACACATGGTGTCAACAACTCCG 907
Db 1005 GCTTCTTCTGATGCTTCCGAGATTCATCTGAGCAACACATGGTGTCTTAAACATCTG 1064
Qy 908 TATGAGA-----TCTTCTGAGTGTATGAAACAGCTACCTGACTT 951
Db 1065 TATGAGATCTTATGCTCTCTTCTGTGTGTGTGAAACAGCTACCTATACCT 1118
RESULT 2
US-10-388-838-11
; Sequence 11, Application US/10388838
; Publication No. US20040180344A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Therapeutic Targets in Cancer
; FILE REFERENCE: 529452001600
; CURRENT APPLICATION NUMBER: US/10/388,838
; CURRENT FILING DATE: 2003-03-14
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 75164
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(75164)
; OTHER INFORMATION: n = A,T,C or G
US-10-388-838-11
Query Match 21.1%; Score 254.8; DB 9; Length 75164;
Best Local Similarity 81.9%; Pred. No. 4e-67;
Matches 349; Conservative 0; Mismatches 57; Indels 20; Gaps 4;
Qy 536 CAGATTCATCCATCCGGGAGAGGAAAGATTTGCTTACTGAAACAACGCGATCAGAG 595
Db 63635 CAGATTCATCCATCCGGGAGAGGAAAGATTTGCTTACTGAAACAACGCGATCAGAG 63694
Qy 596 TACAGGATCTATTCATCTGATGTGATCTGTAGCAAGCTCAACAGCTATAGCTTCA 655

Db 63695 TTCCAGGACATATATACCTCGATATGATCTGTAGCAAGCTTAAACAATATAGCTTCA 63754
Qy 656 CTGCCAAATCTCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 715
Db 63755 CTGCCAAATCT 63811
Qy 716 CTGAGGATCT 775
Db 63812 CTATGGGTCT 63871
Qy 776 TTCTTACATCAAGAAATGAAACCATCATTTTCAATTCATGACAGATTTGTAGGTGTA 835
Db 63872 TTTTAAACCTGCAATGAAACCATCAAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 63925
Qy 836 AATACCTGACT 895
Db 63926 AGA-GACTGCT 63984
Qy 896 CACAAACATCCGTAATGAGA-----TCTTCTGAGTGTATGAAACAGCTACCT 945
Db 63985 TCAAAACATCTGTAATGACATCTTATGCTCTCTCTGTGTGTGTGAAACAGCTACCT 64044
Qy 946 GTACTT 951
Db 64045 ATACCT 64050

RESULT 3
US-09-960-352-14614
; Sequence 14614, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 14614
; LENGTH: 429
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (329), (393)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: 62-LIB34-049-Q1-E1-H6
US-09-960-352-14614
Query Match 13.3%; Score 159.8; DB 3; Length 429;
Best Local Similarity 62.2%; Pred. No. 1.2e-38;
Matches 267; Conservative 0; Mismatches 159; Indels 3; Gaps 1;
Qy 207 ATGCTCTACTGTAGCTGAATTTGCTTTTCTGTTGCTTTGCTTGCACCAACAAGACAGA 266
Db 2 ATACTGTAGCTCTTAATGTGTGACACTTTCGTTCTTCTGCACTGAAACAGAG-- 59
Qy 267 CAGATCCAGTCAACAAGACCTATGCTGCTTGCCTGCAAACTGATTTGAGATTTGAAAT 326
Db 60 -AACAAGACTTAACAAGTTGTATGTACACTGCTCCCAAAAGATGATTTGAGATTTGGAA 118
Qy 327 AATATTTTATTTTCTGAAATCCCAAGTATGACATTTGCCAGGCTTCTGATG 386
Db 119 AAGGTTTATTTTCTGAAAGTCAAGAAATTTGACATTTAGTCAATATATCTGACT 178
Qy 387 GCACAAGGCCCACTAGTCTGTTGACACCAAGATGAGCTGAATTTCTTAATGAGA 446
Db 179 TCAGTGGAGCTGTCTTCTGCTAGTTGAAACTGAGAGAGAGTGAACCTTTCTGACAGA 238

GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 24, 2006, 20:05:24 ; Search time 849 Seconds

(without alignments)
9904.042 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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15: Genesegq2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1206	100.0	1206	4	AAFS8431	AAFS8431 Murine mo
2	711.4	59.0	713	4	AAFS8413	AAFS8413 Murine mo
3	669.4	55.5	862	4	AAFS8432	AAFS8432 Murine mo
4	629.6	52.2	990	4	AAFS8408	AAFS8408 Murine mo
5	629.2	52.2	2232	13	ADR67062	ADR67062 Mouse can
6	554	45.9	1907	4	AAFS8406	AAFS8406 Murine mo
7	500.4	41.5	633	4	AAFS8424	AAFS8424 Murine mo
8	493.4	40.9	721	4	AAFS8411	AAFS8411 Murine mo
9	386.2	32.0	620	4	AAFS8405	AAFS8405 Rat iOCiL
10	364.4	30.2	1628	4	AAFS8428	AAFS8428 Rat iOCiL
11	346.8	28.8	1302	4	AAFS8403	AAFS8403 Rat iOCiL
12	307	25.5	1907	4	AAFS8406	AAFS8406 Murine mo
13	277.6	23.0	738	4	AAFS8404	AAFS8404 Rat iOCiL
14	268.4	22.3	402	4	AAFS8400	AAFS8400 Rat iOCiL
15	254.8	21.1	9862	4	AAFS8407	AAFS8407 Murine can
16	254.8	21.1	75164	13	ADR67061	ADR67061 Mouse can
17	176	14.6	250	3	AAA10130	AAA10130 Rat liver
18	176	14.6	250	6	AAA42154	AAA42154 Rat target

19	159.8	13.3	429	8	ABX49449	ABX49449 Bovine ES
20	144.4	12.0	1305	4	AAFS8416	AAFS8416 Human hOC
21	144.4	12.0	1560	2	AAT91295	AAT91295 Human G52
22	144.4	12.0	1560	10	ADC38663	ADC38663 Human cDN
23	143.8	11.9	820	4	AAFS8436	AAFS8436 Human hOC
24	143.8	11.9	823	3	AAA28176	AAA28176 Human clo
25	143.8	11.9	845	4	AAFS8437	AAFS8437 Human hOC
26	143.8	11.9	850	10	ADDB67551	ADDB67551 Human Lyl
27	143.8	11.9	850	12	ADU93624	ADU93624 cDNA enco
28	143.8	11.9	850	12	ADP12837	ADP12837 Reference
29	143.8	11.9	850	12	ADO20148	ADO20148 Human PRO
30	143.8	11.9	850	13	ADRO6493	ADRO6493 Human LIT
31	143.8	11.9	850	14	ADY19967	ADY19967 DNA enco
32	143.8	11.9	850	14	ADY17709	ADY17709 DNA enco
33	143.8	11.9	850	14	AE811651	AE811651 Human lec
34	143.8	11.9	850	15	AE889843	AE889843 Human LIT
35	143.8	11.9	924	12	ADO21138	ADO21138 Human car
36	143.8	11.9	2353	7	ADR41233	ADR41233 Human CD-
37	143.8	11.9	2536	13	ADR67077	ADR67077 Human can
38	143.8	11.9	2542	13	ADR67079	ADR67079 Human can
39	143.8	11.9	2582	13	ADR67069	ADR67069 Human can
40	143.8	11.9	2595	13	ADR67081	ADR67081 Human can
41	143.8	11.9	2628	13	ADR67067	ADR67067 Human can
42	143.2	11.9	673	7	ADR41251	ADR41251 Human CD-
43	142.8	11.8	399	15	AEF25547	AEF25547 Human LIT
44	142.8	11.8	450	10	ADFI7039	ADFI7039 Human alb
45	142.8	11.8	576	15	AEF25545	AEF25545 Human lec

ALIGNMENTS

RESULT 1	AAFS8431	standard; DNA; 1206 BP.
ID	AAFS8431	
AC	AAFS8431;	
XX		
DT	25-APR-2001	(first entry)
XX		
DE	Murine mOCiL clone coding sequence.	
KW	Osteopontin; mononuclear osteoclast precursor formation inhibition;	
KW	calcitonin; osteoclast inhibitory lectin; OCIL; osteoblast; osteoporosis;	
KW	osteoclast differentiation; bone resorption; primary hyperparathyroidism;	
KW	Paget's disease; rheumatoid arthritis; renal osteodystrophy; murine;	
KW	humoral hypercalcaemia; cancer; ss.	
OS	Mus musculus.	
XX		
PN	MO200105964-A1.	
XX		
PD	25-JAN-2001.	
XX		
PF	19-JUL-2000; 2000MO-AU000864.	
XX		
PR	19-JUL-1999; 99AU-00001675.	
XX		
PA	(SVIN-) ST VINCENTS INST MEDICAL RES.	
PI	Zhou H, Kartsoyianis V, Hu Y, Gillespie MT, Ng KW;	
XX		
DR	WPI; 2001-103148/11.	
XX		
PT	Osteoclast inhibitory lectin nucleic acids and polypeptides are expressed	
PT	on an osteoblast cell surface and used for treating excessive bone	
PT	resorption in conditions such as osteoporosis and Paget's disease.	
XX		
PS	Claim 4; Page 119; 131pp; English.	
XX		
CC	The present invention relates to osteoclast inhibitory lectin coding	
CC	sequences and proteins (OCIL). OCIL is a type II membrane protein which	
CC	is expressed on osteoblast cell surfaces. OCIL inhibits osteoclast	

CC differentiation from haematopoietic cell precursors. OCIL is useful for
 CC creating a condition with excessive bone resorption, including
 CC osteoporosis, primary hyperparathyroidism, Paget's disease, rheumatoid
 CC arthritis, renal osteodystrophy, humoral hypercalcaemia of malignancy and
 CC conditions where cancer has metastasised to the bone
 XX

SQ Sequence 1206 BP; 356 A; 275 C; 267 G; 308 T; 0 U; 0 Other;

Query Match 100.0%; Score 1206; DB 4; Length 1206;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 1 GTGCCCTCAGCTTCAAGTTCAATCCTGTAGTGAACCTCAGCTCCTCAGCTGAGA 60
 QY 61 TGTGTGTCAAAAGGCTTCCCTAAGTGTAGTGTCCACAGGACGCGCAGAGGTAG 120
 DB 61 TGTGTGTCAAAAGGCTTCCCTAAGTGTAGTGTCCACAGGACGCGCAGAGGTAG 120
 QY 121 AAGTGGSTAAATTCCTCCAAAGGAAAGGACGGAACCATCTCCCTGAGCTGTGTGCTA 180
 DB 121 AAGTGGSTAAATTCCTCCAAAGGAAAGGACGGAACCATCTCCCTGAGCTGTGTGCTA 180
 QY 181 AGCTTACTGCTACTATGAGATGATGCTCCTCACTGAGCTGTATTTGCTCTTCTG 240
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 QY 241 TTGCTTTTGACGACAAAGACAAAGACAGATCCCACTGACAAAGACCTATGCTTGTGCC 300
 DB 241 TTGCTTTTGACGACAAAGACAAAGACAGATCCCACTGACAAAGACCTATGCTTGTGCC 300
 QY 301 CGGAAACTGGAGTTGGAGTTGAAATTAATGTTTTTATTTTCTGAAATACCAAGTAAT 360
 DB 301 CGGAAACTGGAGTTGGAGTTGAAATTAATGTTTTTATTTTCTGAAATACCAAGTAAT 360
 QY 361 GGACATTTCCGCGGCTTCTGATGAGCAAGAGGCCCACTAGCTCGTGTGACACAC 420
 DB 361 GGACATTTCCGCGGCTTCTGATGAGCAAGAGGCCCACTAGCTCGTGTGACACAC 420
 QY 421 AGGATGAGCTGAATTTCTTAATGATGATCAAGGCGAATTTTGAATTCCTGATGGCCTGC 480
 DB 421 AGGATGAGCTGAATTTCTTAATGATGATCAAGGCGAATTTTGAATTCCTGATGGCCTGC 480
 QY 481 ACGAAGATGCTGAGACACCTTGAAGTGAAGACACACACTGATTAATTAACACGA 540
 DB 481 ACGAAGATGCTGAGACACCTTGAAGTGAAGACACACACTGATTAATTAACACGA 540
 QY 541 TTCCCATCCGCGGAGAGAAAGATTGCTACTGCTGAACCAACAGGGATCAGAGTACCA 600
 DB 541 TTCCCATCCGCGGAGAGAAAGATTGCTACTGCTGAACCAACAGGGATCAGAGTACCA 600
 QY 601 GGATCTATTTCATCTTGGATGTGATCTGACAGCTCAACAGCTATAGCCTCCACTGCC 660
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 QY 661 AAACCTCTTTTTCCTTCCCTAGCATTTACCAAGAGCGCTTTTACCTGTTATCTGTG 720
 DB 661 AAACCTCTTTTTCCTTCCCTAGCATTTACCAAGAGCGCTTTTACCTGTTATCTGTG 720
 QY 721 GGTGCTACTCTTCCCTATGATGCCAAAGTGCATCAACAGATGAGATATTTCTT 780
 DB 721 GGTGCTACTCTTCCCTATGATGCCAAAGTGCATCAACAGATGAGATATTTCTT 780
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 DB 781 AACATGAGAAATGAAAAACATCAATTTTCATGACAGAGATTTTCAGTGTAAATC 840
 QY 841 ACGAATCACTCTCCGAGGCTGAGTTCAATCTGAGAACCAACATGTGTGCTCAAA 900
 DB 841 ACGAATCACTCTCTCCGAGGCTGAGTTCAATCTGAGAACCAACATGTGTGCTCAAA 900
 QY 901 ACATCCGTAATGAGATCTTCTGAGGTGTATGAAAAACAGTACACTGTATTAATCTCTG 960

DB 901 ACATCCGTAATGAGATCTTCTGAGGTGTATGAAAAACAGTACACTGTATTAATCTCTG 960
 QY 961 CAATTTAAAGCATGAGGACATGAGAGATTTGCTTACCCACACTATAGTATCCAAAA 1020
 DB 961 CAATTTAAAGCATGAGGACATGAGAGATTTGCTTACCCACACTATAGTATCCAAAA 1020
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 DB 1021 GGACGAAATATACAGGCTTAAAGACCTCTTGAACCTCTTCATCTCTTCTCCCTCTTG 1080
 QY 1081 GTCTTTTAAAGCCAGGTCGCTGAGAGAAAAGATGAGAAATGGGAAAGGAGG 1140
 DB 1081 GTCTTTTAAAGCCAGGTCGCTGAGAGAAAAGATGAGAAATGGGAAAGGAGG 1140
 QY 1141 GAGAGGACATGATTTGGGAGAGGAGGAGGAAAGAAATTAATTAATTAATTAATTAAT 1200
 DB 1141 GAGAGGACATGATTTGGGAGAGGAGGAGGAAAGAAATTAATTAATTAATTAATTAAT 1200
 QY 1201 TACTAC 1206
 DB 1201 TACTAC 1206

RESULT 2
 AAF58413
 ID AAF58413 standard; DNA; 713 BP.

AAF58413;
 DT 25-APR-2001 (first entry)

XX Murine MOCIL17 clone coding sequence #1.

XX Osteopathic; mononuclear osteoclast precursor formation inhibition;
 XX calcitonin; osteoclast inhibitory lectin; OCIL; osteoblast; osteoporosis;
 KW osteoclast differentiation; bone resorption; primary hyperparathyroidism;
 KW Paget's disease; rheumatoid arthritis; renal osteodystrophy; murine;
 KW humoral hypercalcaemia; cancer; ss.

XX Mus musculus.

OS WO200105964-A1.

PN 25-JAN-2001.

PD 19-JUL-2000; 2000WO-AU000864.

PF 19-JUL-1999; 99AU-00001675.

PR (SVIN-) ST VINCENTS INST MEDICAL RES.

PA Zhou H, Kartsojiannis V, Hu Y, Gillespie MT, Ng KW;

PT WPI; 2001-103148/11.

XX Osteoclast inhibitory lectin nucleic acids and polypeptides are expressed
 PT on an osteoblast cell surface and used for treating excessive bone
 PT resorption in conditions such as osteoporosis and Paget's disease.

XX Example 11; Page 109; 131p; English.

XX The present invention relates to osteoclast inhibitory lectin coding
 CC sequences and proteins (OCIL). OCIL is a type II membrane protein which
 CC is expressed on osteoblast cell surfaces. OCIL inhibits osteoclast
 CC differentiation from haematopoietic cell precursors. OCIL is useful for
 CC treating a condition with excessive bone resorption, including
 CC osteoporosis, primary hyperparathyroidism, Paget's disease, rheumatoid
 CC arthritis, renal osteodystrophy, humoral hypercalcaemia of malignancy and
 CC conditions where cancer has metastasised to the bone

SQ Sequence 713 BP; 190 A; 179 C; 157 G; 187 T; 0 U; 0 Other;

GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 24, 2006, 20:59:59 ; Search time 31 Seconds
(without alignments)
4391.567 Million cell updates/sec

Title: US-10-031-902A-36

Perfect score: 1206

Sequence: 1 gggccctcagcttcacagt.....aataaaccacaaatactac 1206

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IDENTITY_NUC
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Searched: 242596 seqs, 56442199 residues

Total number of hits satisfying chosen parameters: 485192

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
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Published Applications NA New:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
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2	76.4	6.3	553	6	US-10-488-619-1138	Sequence 1138, Ap
3	76.4	6.3	577	6	US-10-488-619-1139	Sequence 1139, Ap
4	75.6	6.3	1702	6	US-10-511-937-429	Sequence 429, App
5	75.6	6.3	1702	6	US-10-511-937-2866	Sequence 2866, Ap
6	74	6.1	820	6	US-10-488-619-2550	Sequence 2550, Ap
7	70.6	5.9	697	6	US-10-488-619-1108	Sequence 1108, Ap
8	67	5.6	732	6	US-10-196-749-577	Sequence 577, App
9	62.2	5.2	586	6	US-10-488-619-1067	Sequence 1067, App
10	62.2	5.2	721	6	US-10-488-619-1109	Sequence 1109, Ap
11	59	4.9	575	6	US-10-488-619-1066	Sequence 1066, Ap
12	54.6	4.5	798	6	US-10-488-619-2237	Sequence 2237, Ap
13	52.2	4.3	876	6	US-10-488-619-2828	Sequence 2828, Ap
14	49.2	4.1	565	6	US-10-488-619-1983	Sequence 1983, Ap
15	49	4.1	347	6	US-10-488-619-1731	Sequence 1731, Ap
16	47.2	3.9	896	7	US-11-268-890-3	Sequence 3, App1
17	47.2	3.7	22118	7	US-11-284-877-16	Sequence 16, App1
18	44.8	3.5	2468	7	US-11-293-697-1278	Sequence 1278, App
19	42	3.5	42999	7	US-10-488-619-1349	Sequence 1349, App
20	38.4	3.2	712	6	US-10-519-335-37	Sequence 37, App1
21	37	3.1	151830	6	US-10-511-937-376	Sequence 376, App
22	35.6	3.0	2378	6	US-10-953-349-26450	Sequence 26450, A
23	35.4	2.9	1362	6	US-10-953-349-9480	Sequence 9480, App
24	35.4	2.9	2907	7	US-11-145-307A-200	Sequence 200, App
25	34.8	2.9	784	6	US-10-488-619-2056	Sequence 2056, App

26	34.2	2.8	1836	6	US-10-953-349-10090	Sequence 10090, A
27	34	2.8	10211	6	US-10-505-928-326	Sequence 326, App
28	33.6	2.8	1800	6	US-10-505-928-78	Sequence 78, App1
29	33	2.7	2378	7	US-11-293-697-1075	Sequence 1075, App1
30	32.8	2.7	406	6	US-10-488-619-2489	Sequence 2489, Ap
31	32.4	2.7	1110	7	US-11-217-529-79308	Sequence 79308, A
32	32.4	2.7	1413	7	US-11-217-529-79045	Sequence 79045, A
33	32	2.7	135090	6	US-10-505-928-607	Sequence 607, App
34	31.8	2.6	484	6	US-10-488-619-1014	Sequence 1014, App
35	31.8	2.6	987	6	US-10-519-335-37	Sequence 37, App1
36	31.8	2.6	151830	6	US-10-511-937-518	Sequence 518, App
37	31.6	2.6	1449	6	US-10-511-937-376	Sequence 376, App
38	31.6	2.6	1812	6	US-10-953-349-6676	Sequence 6676, App
39	31.6	2.6	1847	6	US-10-511-937-376	Sequence 376, App
40	31.6	2.6	2610	6	US-10-953-349-1990	Sequence 1990, App
41	31.2	2.6	1250	6	US-10-953-349-5096	Sequence 5096, App
42	31.2	2.6	1278	6	US-10-953-349-5096	Sequence 5096, App
43	31.2	2.6	3219	7	US-11-293-697-1221	Sequence 1221, App1
44	31.2	2.6	42989	7	US-11-284-877-17	Sequence 17, App1
45	31.2	2.6	394191	6	US-10-506-549-3	Sequence 3, App1

ALIGNMENTS

RESULT 1
US-10-511-937-2846
Sequence 2846, Application US/10511937
Publication No. US200608836A1
GENERAL INFORMATION:
APPLICANT: EXPRESSION DIAGNOSTICS, INC.
APPLICANT: Wohlgemuth, Day
APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
APPLICANT: Ly, Ngoc
APPLICANT: Prentice, James
APPLICANT: Morris, Macdonald
APPLICANT: Rosenberg, Steven
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
FILE REFERENCE: 50661200104
CURRENT APPLICATION NUMBER: US/10/511.937
CURRENT FILING DATE: 2004-10-19
PRIOR APPLICATION NUMBER: PCT/US2003/012946
PRIOR FILING DATE: 2003-04-24
PRIOR APPLICATION NUMBER: US 10/131,831
PRIOR FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: US 10/325,899
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 3117
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2846
LENGTH: 850
TYPE: DNA
ORGANISM: Homo sapiens
US-10-511-937-2846

Query Match 11.9%; Score 143.8; DB 6; Length 850;
Best Local Similarity 62.7%; Pred. No. 7.2e+34;

Matches 259; Conservative 0; Mismatches 147; Indels 7; Gaps 2;

QY	289	ATGTCCTGTCGCCGCAAACTGATGAGTTGAAATAATGTTTATTTTCGAA	348
QY	228	AAGCTCAGCCAGCAAGCTGATGTTTCAAGAAAGTCTTCATTTTCGANG	287
DB	349	ACCAAGTACAGGATTCGCCAGCTTCGATGCAAGAGGCCCACTGAC	408
DB	288	ACACCAAGTACAGGATTCGCCAGCTTCGATGCAAGAGGCCCACTGAC	347
QY	409	GGTTTGACCAAGAGTGAATTTCTATGATGACCAAGGCAATTTTATTCCT	468
DB	348	AGGTTTAAAGCTTCAGCAAGTGAATTTCTGTTGATGATTAAGGCCCATGATCACT	407

Oy	469	GGATTGGGCTGCA	CAGAGAGTGTGT	CAGAGACCCCTTGGAA	GTGACAGACAACTGAGT	528
Db	408	GGATTGGGCTGAG	CACAGAG---ACAAGGCC	CAACCAATGGAAATGGTACTGGAAT		464
Oy	529	ATTAACAACAGAT	TTTCCCATCCGCGGG	GAGAGAAAGATTGGCTCACTGAA	CAACAACAGCGGA	588
Db	465	GGACAAGACAGT	TTTCTTATCTCTGGAG	CAGAGAGTGTGCTATTTGAATGACAAAGTG		524
Oy	589	TCAGCAGTACAG	AGATCTATTCACTT	CGAGTGTGATCTGTAGCA---AGTC	CAACAGC	644
Db	525	CCAGTAGTGCC	CAGGCACTACACAG	AGAGGAAGTGGAATTTGTTCCAAATCAGATATACATG		584
Oy	645	TATAGCTCCACT	GGCAACTCTTTTTCCTT	CCTAGATTTTACCAAGAGA		697
Db	585	TCTATATGTTTAC	AGCAAAAGCCCCCACTAATCTTT	TGAAGATATGTGAACTGA		637

```

RESULT 2
US-10-488-619-1138/C
; Sequence 1138, Application US/10488619
; Publication No. US2006009578A1
; GENERAL INFORMATION:
; APPLICANT: Greentree, winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; TITLE OF INVENTION: Physiological Conditions, And Genotyping Arrays
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488, 619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1138
; LENGTH: 553
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-488-619-1138

```

	Query Match	6.3%	Score 76.4;	DB 6;	Length 553;
	Best Local Similarity	75.7%;	Pred. No. 1.1e-13;		
	Matches 112;	Conservative 0;	Mismatches 26;	Indels 10;	Gaps 1;
QY	814	TGCAGAGATTGTTTCAGTGGTTAAATCATCTACTCTCCGAAGGCTCGAGTTACA			873
Db	175	TGGCAAGACGGCTTCAGCAGGTTAAGCACTACTTTCTTCCAAAGTCTCGAGTTCAA			116
QY	874	TCTGAGCAACCATGATGGTCTCACAAACATCCGTAATGAGA-----TCTTCTGA			923
Db	115	TCCGAGCAACCATGATGGTCTCACAAACCATTAATGAGATTCGAGCCCTTCTTGG			56
QY	924	GGTATATGAAAACAGCTACACTGTACTT			951
Db	55	TATGTCTGAAGCACGCTACAGTACTT			28

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RESULT 3
US-10-488-619-1139
; Sequence 1139, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; TITLE OF INVENTION: Physiological Conditions, And Genotyping Arrays
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: Patencin version 3.1
; SEQ ID NO 1139
; LENGTH: 577
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-488-619-1139

```

Query Match 6.3%; Score 76.4; DB 6; Length 577;

	Best Local Similarity	75.7%	Pred. No. 1,je-13:	Matches 112:	Conservative 0:	Mismatches 26:	Indels 10:	Gaps 1
OY	814	TCGACAGATTGTTGAGTGGTTAAATATCATCTGACTACTTTTCCGAAGGTCCTGAGTTTACA	873					
Db	424	TGGCAAGCGGCTCAGCAGGTAAAGCATGACTGTTTCCAAAGGTCCTGAGTTCAA	483					
OY	874	TCTGAGCAACACATGTTGGCTCTCAAAACATCCGTATGAGA-----TCTTTCTGA	923					
Db	484	TCCAGACACCATGTTGGCTCTCAACACCATATATGAGATTGACGCTTCTTTCTGG	543					
OY	924	GGTGTATGAAAACGCTACACTGACTT	951					
Db	544	TATGTTGAAAGACACTACAGTTGACTT	571					

```

RESULT 4
US-10-511-937-429
; Sequence 429, Application US/10511937
; Publication No. US20060088836a1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: METHODS AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 429
; LENGTH: 1702
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-511-937-429

```

Query Match	6.3%	Score 75.6	DB 6	Length 1702
Best Local Similarity	51.0%	Pred. No. 3.5e-13		
Matches 205	Conservative 0	Mismatches 194	Indels 3	Gaps 1
QY	245	TTTGTGACCAACAAGACAGCAACATCCCAAGCTAAAGACCTATGCTTGTCGCCCGCA	304	
Db	282	TTGTCCAGGCCAAATACATCTCTCATGTGCACACAGCGCCATGTTCTTCAATGCTCTGA	341	
QY	305	AAACTGATGTGGAGTTGAAATAATTAATGTTTTTATTTTCTGATATCCCAAGTAACTCGAC	364	
Db	342	GGACTGGGTTGGCTACCAAGGAATGCTACTTATTTTCTATGTGAAAGACAGCTGGAC	401	
QY	365	ATTGCGCCAGGCTTCTGCATGTGCAAGAGGCCCAACTAGTCCGTTTGACAACCGAGA	424	
Db	402	TTCAACCCAAATGCTGTGTTCTGAAACATGTGCTACTCTGTCTGTCATTTGTAATAA	461	
QY	425	TGAGCTGAATTTCTTAATGAGATACAAAGCGCAATTTGATTTCTTGATTTGGCTGCACAG	484	
Db	462	GGACCTGGAATCTTTCTTAAAAACGATACGAGTGAAGAGGAACACTGGGTGGACATG--AA	518	
QY	485	AGAGTGTCACAGCAACCTTGGAACTGGACACAGCAACAACGTAGTATTAACAACGCAATTC	544	
Db	519	AAAGGAACCTGTCTACCCATGGAATGGTGCCTAAATGGCCAAAGAATTTAAACAACCTGGTTCAA	578	
QY	545	CATCCGGGGAGAGGAAGAATTTGCTACTCTGAACAACAACGGGATCAGCATACCAGAT	604	

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OM nucleic - protein search using frame n2p model

Run on: May 23, 2006, 15:44:38 ; Search time 44.5 Seconds
(without alignments)
3717.324 Million cell updates/sec

Title: US-10-031-902A-36

Perfect score: 2160
Sequence: 1 gtccctcctcagcttcacgc.....aataaacaataactac 1206

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 5179358

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODE=frame+ n2p.model -DEV=xlp
-O=/abs/ABSSWB.spool/US10031902/runat.23052006.145339.461/app.query.fasta.1
-DB=A.Geneseq -OPMT=fastan -SUFFIX=n2p.rag -MINMATCH=0.1 -LOOPCT=0 -LOOPEXT=0
-UNITS-bits -START=1 -END=1 -MATRIX=blomum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pro -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abs02p
-USER=US10031902.OCGN.1.1.364@runat.23052006.145339.461 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-MARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

A_Geneseq_8: *
1: geneseqp1980s: *
2: geneseqp1990s: *
3: geneseqp2000s: *
4: geneseqp2001s: *
5: geneseqp2002s: *
6: geneseqp2003as: *
7: geneseqp2003bs: *
8: geneseqp2004s: *
9: geneseqp2005s: *
10: geneseqp2006s: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1125	52.1	207	4	AAB68583	Aab68583 Murine mo
2	1125	52.1	207	8	ADJ58739	Adj58739 Mouse DCA
3	861.5	39.9	281	8	ADJ67063	Adj67063 Mouse can
4	799	37.0	218	4	AAB68584	Aab68584 Murine mo
5	725	33.6	217	4	AAB68585	Aab68585 Murine mo
6	377	17.5	191	4	AAB68586	Aab68586 Human hOC
7	376	17.4	191	7	ADJ67552	Adj67552 Human Ly1
8	376	17.4	191	8	ADJ93621	Adj93621 Human lec

9	376	17.4	191	8	ADJ58738	Adj58738 Human DCA
10	376	17.4	191	8	ADP12932	Adp12932 Protein e
11	376	17.4	191	8	ADO20149	Ado20149 Human PRO
12	376	17.4	191	8	ADRO6494	Adro6494 Human LIT
13	376	17.4	191	8	ADRG6708	Adrg6708 Human can
14	376	17.4	191	9	ADY17710	Ady17710 PRO polyP
15	376	17.4	191	9	ADY19968	Ady19968 PRO polyP
16	376	17.4	191	9	AEBl1652	Aebl1652 Human lec
17	376	17.4	191	10	AEER89840	Aeer89840 Human LIT
18	376	17.4	191	10	AEF25546	Aef25546 Human lec
19	376	17.4	272	3	AAV94741	Aav94741 Human clo
20	373.5	17.3	181	2	AAW27288	Aaw27288 Human G52
21	373.5	17.3	181	7	ADC3664	Adc3664 Human sec
22	368.5	17.1	149	7	ADFI17049	Adfi17049 Human alb
23	368.5	17.1	149	8	ADRG67070	Adrg67070 Human can
24	359	16.6	184	5	ADRA41427	Adra41427 Human CD-
25	351.5	16.3	739	7	ADFI17045	Adfi17045 Human alb
26	347	16.1	328	3	AAV94744	Aav94744 Murine CD
27	345.5	16.0	132	10	AEER89842	Aeer89842 Human LIT
28	345.5	16.0	154	8	AEF25548	Aef25548 Human LIT
29	345.5	15.9	137	4	ADJ93623	Adj93623 C-termina
30	342.5	15.9	137	4	AAAB68578	Aaab68578 Murine mo
31	338.5	15.7	288	3	AAV94740	Aav94740 Human clo
32	317	14.7	188	9	AEAR6021	Aear6021 Chicken M
33	304	14.1	188	5	ADRA41551	Adra41551 Human CD-
34	293.5	13.6	187	5	AAW85594	Aaw85594 Chicken 1
35	292	13.5	257	2	AAV94739	Aav94739 Human c-1
36	291	13.5	194	3	AAAB74702	Aaab74702 Human mem
37	291	13.5	199	4	AAAR54659	Aaar54659 Human CD6
38	291	13.5	199	2	AAW85593	Aaw85593 Human CD6
39	291	13.5	199	7	ADJ58741	Adj58741 Human DCA
40	291	13.5	199	8	ADL82855	Adl82855 Human PRO
41	291	13.5	199	8	ADP12478	Adp12478 Protein e
42	291	13.5	199	8	ADP12916	Adp12916 Protein e
43	291	13.5	199	8	ADP12916	Adp12916 Protein e
44	291	13.5	199	8	ADP12916	Adp12916 Protein e
45	291	13.5	199	8	ADP12916	Adp12916 Protein e

ALIGNMENTS

RESULT 1	ADJ58738	standard; protein; 207 AA.
ID	AAB68583	
XX	XX	
AC	AAB68583;	
XX	XX	
DT	25-APR-2001	(first entry)
XX	XX	
DE	Murine mOCIL.	
XX	XX	
KW	Osteopathic; mononuclear osteoclast precursor formation inhibition;	
KW	calcitonin; osteoclast inhibitory lectin; OCIL; osteoblast; osteoporosis;	
KW	osteoclast differentiation; bone resorption; primary hyperparathyroidism;	
KW	Paget's disease; rheumatoid arthritis; renal osteodystrophy; murine;	
KW	humoral hypercalcemia; cancer.	
OS	Mus musculus.	
XX	XX	
PN	W0200105964-AL.	
XX	XX	
PD	25-JAN-2001.	
XX	XX	
PF	19-JUL-2000; 2000WO-AU000864.	
XX	XX	
PR	19-JUL-1999; 99AN-00001675.	
PA	(SVIN-) ST VINCENTS INST MEDICAL RES.	
XX	XX	
PI	Zhou H, Kartsoyannis V, Hu Y, Gillespie MT, Ng KW;	
XX	XX	
DR	WPI; 2001-103148/11.	
XX	XX	

PT Osteoclast inhibitory lectin nucleic acids and polypeptides are expressed
 PT on an osteoblast cell surface and used for treating excessive bone
 PT resorption in conditions such as osteoporosis and Paget's disease.

XX Disclosure, Fig 8, 131pp, English.

XX The present invention relates to osteoclast inhibitory lectin coding
 CC sequences and proteins (OCIL). OCIL is a type II membrane protein which
 CC is expressed on osteoblast cell surfaces. OCIL inhibits osteoclast
 CC differentiation from haematopoietic cell precursors. OCIL is useful for
 CC treating a condition with excessive bone resorption, including
 CC osteoporosis, primary hyperparathyroidism, Paget's disease, rheumatoid
 CC arthritis, renal osteodystrophy, humoral hypercalcaemia of malignancy and
 CC conditions where cancer has metastasised to the bone

XX Sequence 207 AA;

Alignment Scores:

Pred. No.:	1.02e-102	Length:	207
Score:	1125.00	Matches:	207
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	52.1%	Indels:	0
DB:	4	Gaps:	0

US-10-031-902A-36 (1-1206) x AAB68583 (1-207)

QY 60 ATGTGTGTCAAAAGGCTTCCCTACTATGCTTAGTCCACAGAGCCCGGAGAGGTA 119

DB 1 MetCysValThrIysAlaSerLeuProMetLeuSerProThrIleSerProGlnGluVal 20

QY 120 GAAGTGGTAAATTTCTCCAGGAAAAGGACGAGAACCTCTCCCTGAGTCTTGCT 179

DB 21 GluValGlyLysIleLeuGlnGlyLysArgHisGlyThrIleSerProGlnGluVal 40

QY 180 AAGCTTTACTGCTACTACTAGATGATCATGCTCTCACTAGCTGTGATTTGCTTTCT 239

DB 41 LysLeuIleCysIleValIleMetValIleThrAlaIleAlaIleAlaLeuSer 60

QY 240 GTTGTCTTTGTACAGCAAAAGACAGATCCCACTCAACAGAGCTTAGCTGCTTC 239

DB 61 ValAlaLeuSerIleThrIleGlnIleProValAsnIleThrIleAlaIleCys 80

QY 300 CCGCAAACTGATGATGAGTGAATAATGTTTATTTCTGAAATACCCAGATTAAC 359

DB 81 ProGlnAsnTrpIleGlyValIleAsnIleCysPheIleIleIleIleIleIleIle 100

QY 360 TGGACATTCGCCCGAGGCTTCTGCATGAGCAAGAGGCCCACTAGCTCGGTTGACAC 419

DB 101 TrpThrPheAlaGlnIlePheCysMetAlaGlnIleValIleAlaIleAlaIleAspAsn 120

QY 420 CAGGATGAGCTGAATTTCTTAATGAGATACAGGCCAATTTTATTTCTGATTTGCGCTG 479

DB 121 GlnAspGlnLeuAsnPheLeuMetArgIleValAlaAsnIleAspSerTrpIleGlyLeu 140

QY 480 CACAGAGAGTCCGACAGACACCTTGGAGTGGACAGACACTGAGTTAAACACAGC 539

DB 141 HisArgGlnSerSerGlnIleIleIleIleIleIleIleIleIleIleIleIleIle 160

QY 540 ATTCCCATCCGGGAGAGAAAGATTTCCTACTGTAACAACAACGGGATCAGACAGTACC 599

DB 161 IleProIleArgIleGlyGlnIleArgPheAlaIleIleAsnIleAsnIleIleSerSerThr 180

QY 600 AGGATCTATTCACTTGGAGTGGATGTGAGCAAGCTCAACAGCTTAGCTTCCACTGC 659

DB 181 ArgIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 200

QY 660 CAACACTCTTTTCTTCTTCC 680

DB 201 GlnThrProPheProSer 207

RESULT 2
ADJ58739

ID ADJ58739 standard; protein; 207 AA.

XX AC ADJ58739;

XX DT 06-MAY-2004 (first entry)

XX DE Mouse DCAL-Hy protein carbohydrate recognition domain (CRD) #1.

XX KW Type II C-type lectin-like homologue; DCAL-Hy protein; medicament;

XX KW B-cell neoplasm; cancer; drug screening; vaccine; gene therapy;

XX KW cytosolic; mouse.

XX OS Mus musculus.

XX PN US2004005592-A1.

XX PD 08-JUN-2004.

XX PF 03-MAR-2003; 2003US-00379127.

XX PR 05-MAR-2001; 2001US-00799451.

XX PA (EMTA/) EMTAGE P C R.

XX PA (DRMA/) DRMANAC R T.

XX PA (GOOD/) GOODRICH R W.

XX PA (TANG/) TANG Y T.

XX PI Emtage PCR, Drmanac RT, Goodrich RW, Tang YT;

XX DR WPI; 2004-167523/16.

XX PT New human DCAL-Hy polypeptides and encoding nucleic acid molecules,

XX PT useful for diagnosing, preventing or treating B-cell neoplasm (e.g.

XX PT lymphoma) and in research applications or in drug screening assays.

XX PS Disclosure; SEQ ID NO 24; 87pp; English.

XX CC The present invention relates to novel type II C-type lectin-like

XX CC homologues, including variants, denoted herein as DCAL-Hy 1-5 and

XX CC collectively known as DCAL-Hy proteins and polynucleotides encoding such

XX CC proteins. The nucleic acid molecules, polypeptides, anti-DCAL-Hy

XX CC antibodies or antigen-presenting cells are useful in preparing a

XX CC medicament or vaccine for killing or inhibiting the growth of DCAL-Hy-

XX CC expressing cells that cause B-cell neoplasm. The polynucleotides and

XX CC polypeptides may also be used in diagnosing or preventing cancer, in

XX CC research applications or in drug screening assays. They are used as

XX CC vaccines and in gene therapy. The present sequence is mouse DCAL-Hy

XX CC protein carbohydrate recognition domain (CRD) domain.

XX SQ Sequence 207 AA;

Alignment Scores:

Pred. No.:	1.02e-102	Length:	207
Score:	1125.00	Matches:	207
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	52.1%	Indels:	0
DB:	8	Gaps:	0

US-10-031-902A-36 (1-1206) x ADJ58739 (1-207)

QY 60 ATGTGTGTCAAAAGGCTTCCCTACTATGCTTAGTCCACAGAGCCCGGAGAGGTA 119

DB 1 MetCysValThrIysAlaSerLeuProMetLeuSerProThrIleSerProGlnGluVal 20

QY 120 GAAGTGGTAAATTTCTCCAGGAAAAGGACGAGAACCATCTCCCTGAGTCTTGCT 179

DB 21 GluValGlyLysIleLeuGlnGlyLysArgHisGlyThrIleSerProGlnGluVal 40

QY 180 AAGCTTTACTGCTACTACTAGATGATCATGCTCTCACTAGCTGTGATTTGCTTTCT 239

DB 41 LysLeuIleCysIleValIleMetValIleThrValAlaIleAlaIleAlaLeuSer 60

GenCore version 5.1.8
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OM nucleic - protein search, using frame_plus_n2p model

Run on: May 23, 2006, 15:52:34 ; Search time 10.3 Seconds
(without alignments)
3379.731 Million cell updates/sec

Title: US-10-031-902A-36
Perfect score: 2160
Sequence: 1 gfgcctcctcgccttcaagf.....aataaaccacaataactac 1206

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODE=frame+n2p.model -DEV=xlp
-Q=abs/ABSSWB.spool/US10031902/rnatc.23052006.145347.561/app.query.fasta_1
-DB=PIR -OPMT=faatan -SUFFIX=n2p.rpr -MINMATCH=0.1 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTPMT=pco -NOR=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abs02p
-USER=US10031902.@CGA_1.1.63@unat.23052006.145347.561 -NCP=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-MARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
1: pir.80:*
2: pir1:*
3: pir2:*
4: pir3:*
5: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	304	14.1	156	2	T28141	C type lectin, B1
2	292	13.5	257	2	T50146	gene 17.5 protein
3	281	13.5	189	2	UH0822	lymphocyte early a
4	200	9.3	223	2	B46467	NKR-p1 protein hom
5	190.5	8.8	220	2	C46467	NKR-p1 protein hom
6	190.5	8.8	224	2	S29855	asialoglycoprotein
7	183	8.5	550	2	A28166	Kupffer cell recep
8	182.5	8.4	225	2	I38700	NKR-p1a protein -
9	179.5	8.3	223	2	A35917	NK-cell receptor p
10	176.5	8.2	304	2	TX0309	lectin, galactose/
11	174.5	8.1	221	2	PT0374	natural killer cel
12	174	8.0	227	2	A46467	natural killer cel
13	173	8.0	301	2	S13165	asialoglycoprotein
14	168.5	7.8	216	2	PT0375	natural killer cel

15	168	7.8	284	1	LNRTU	hepatic lectin - r
16	168	7.8	301	1	LNRT2	hepatic lectin 2 -
17	167	7.7	233	2	PT0372	natural killer cel
18	166	7.7	311	1	LNH02A	asialoglycoprotein
19	165.5	7.7	321	1	LNH02A	IGF Fc receptor II
20	165.5	7.7	331	1	LNH02A	IGF Fc receptor II
21	165	7.6	291	1	LNH02A	hepatic lectin H1
22	161.5	7.5	309	1	S34198	IGF Fc receptor II
23	161	7.5	240	2	I54524	natural killer cel
24	159.5	7.4	404	2	A46274	HIV gp120-binding
25	157.5	7.3	306	2	A42230	lectin M-ASGP-BP p
26	154.5	7.2	170	2	T28140	natural killer cel
27	153	7.1	237	2	JC7608	type II lectin-lik
28	151	7.0	267	2	I55686	LDL-1 - mouse
29	150	6.9	207	1	LNCHL	hepatic lectin - c
30	149.5	6.9	267	2	I49053	ly-49G.2 antigen -
31	149	6.9	363	2	JE0111	lectin-like oxidiz
32	148.5	6.9	167	1	MMVZP8	hepatic lectin hom
33	145.5	6.7	116	1	MMVZP8	hepatic lectin hom
34	145	6.7	280	2	I49052	ly-49G.1 antigen -
35	144.5	6.7	552	2	C96563	probable protein k
36	142	6.6	266	2	I49059	Ly49c - mouse
37	140	6.5	321	2	T26152	hypothetical prote
38	140	6.5	1456	1	A36563	mannose receptor p
39	136.5	6.3	163	1	A34313	antifreeze protein
40	135	6.2	266	2	I49363	natural killer cel
41	133.5	6.2	742	2	JC7595	scavenger receptor
42	133.5	6.2	990	2	H88733	protein F32E10.3 {
43	131	6.1	262	2	A45813	T-cell surface gly
44	130	6.0	146	2	JC7105	aggreclin beta chai
45	130	6.0	262	2	I49361	natural killer cel

ALIGNMENTS

RESULT 1
T28141
C type lectin, B locus - chicken
C/Species: Gallus gallus (chicken)
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
R/Mline, S.: Kaufman, J.; Beck, S.
Submitted to the EMBL Data Library, May 1998
A/Description: DNA sequencing and analysis of the chicken major histocompatibility comp
A/Reference number: Z20475
A/Accession: T28141
A/Status: preliminary; translated from GB/EMBL/DBD
A/Molecule type: DNA
A/Residues: 1-156 <MIL>
A/Cross-references: UNIPARC:UPI00011F63F; EMBL:AL023516; NTD:e1292539; PID:e1292545; P
A/Experimental source: clone CB12
C/Genetics:
A/Map position: 16
A/Intons: 17/1; 74/3; 110/2

Alignment Scores:
Pred. No.: 2.08e-21
Score: 304.00
Percent Similarity: 55.4%
Best Local Similarity: 37.3%
Query Match: 14.1%
DB: 2
Gaps: 3

US-10-031-902A-36 (1-1206) x T28141 (1-156)

QY 210 GTCCTCAGTACCTGAAATTT---GCTCTTCTGTTGCTTGTGCAGCAACAAGACGAA 266
DB 4 ValpetherValleuenuillethraValaAlaAphaValaValaAlaAphaGlnProHis 23
QY 267 CAGATCCAGTCAACAAGACCTATGCTGCTTGCCTGCCCAAACTGATTTGAAAT 326
DB 24 ProGlnProGly-----AlaGlnGlyProPheAspTrpIleGlyPheArgGly 39

```
QY 327 AAATGTTTATTTTTCGAATACCAAGTAATGGACATTTGGCCAGGCTTTCGATG 386
    |||:::|||||
Db 40 LysCysTyrTyrPheSerGlnSprGlnSerAsnTrpThrSerSerGlnAsnGlySer 59
    |||:::|||||
QY 387 GCACAGAGAGCCCACTAGCTCGTTTGAACAACAGATGAGCTGAATTTCTTAATGAGA 446
    |||:::|||||
Db 60 AlaLeuGlyAlaSerLeuAlaValPheAspSerAlaGlnAspLeuSerPheThrMetAla 79
    |||:::|||||
QY 447 TACAAAGGCAATTTTATTCCTGGATTGGCTTCACAGAGAGTGTGCAGAGCACCTTGG 506
    |||:::|||||
Db 80 HisLysGlySerSerProHisTrpValGlyLeuSerArgGlnGlyLysGlnHisProTyr 99
    |||:::|||||
QY 507 AAGTGACAGACACACCTAGTATTAACAACACAGATTCACATCCAGGGAGAAAGATT 566
    |||:::|||||
Db 100 GlnTrpValAsnArgSerProLeuSerHisLeuPheGlnValGlnGlnArgGlyLeuGly 119
    |||:::|||||
QY 567 GCCTACCTGAACAACAACGAGATCAGACATGACAGATCTTATTCACCTTGGATGGATC 626
    |||:::|||||
Db 120 AlaTyrLeuGlyAspAlaGlyLeuSerSerSerHisCysSerThrArgGlnGlnTrpVal 139
    |||:::|||||
QY 627 TGTAGCAAGCTCAACAGCTATAGCTTCACCTGACCAACTCTTTTCTTCTCTAGAT 686
    |||:::|||||
Db 140 CysThrLys-----ProAlaLeuGln 146
    |||:::|||||
QY 687 TTACCAAGAGAGCGCTTTT 704
    |||:::|||||
Db 147 LysProAlaGlyAsnPhe 152
    |||:::|||||

RESULT 2
150146
gene 17.5 protein - chicken
C:Species: Gallus gallus (chicken)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: I50146
R:Bernot, A.; Zoorob, R.; AufRAY, C.
Immunogenetics 39, 221-229, 1994
A:Title: Linkage of a new member of the lectin supergene family to the chicken Mhc genes
A:Reference number: I50146; MIMD:94154691; PMID:8119728
A:Accession: I50146
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-257 <DB>
A:Cross-references: UNIPROT:Q90636; UNIPARC:UPI000006B14E; GB:M88072; NID:G505324; PIDN:
F:129-241/Domain: C-type lectin homology <LCH>

Alignment Scores:
Pred. No.: 3.32e-20 Length: 257
Score: 292.00 Matches: 65
Percent Similarity: 54.6% Conservative: 36
Best Local Similarity: 35.1% Mismatches: 71
Query Match: 13.5% Indels: 13
DB: 2 Gaps: 5

US-10-031-902A-36 (1-1206) x I50146 (1-257)
QY 101 AGGACGCCGACGAGGTAGTAAGTGGGTAATTTCTCCAAGAAAGACGAGAACCAT 160
    |||:::|||||
Db 74 ArgGlnSerGlnArgGly--SerGlyCysSerGlnLeuArgGlnAsnA-gArgArg-- 91
    |||:::|||||
QY 161 CTCCTCGAGCTTGTGCTAAGCTTTTACTACTACTATGATGAGTGCATGGTCTCACTGT 220
    |||:::|||||
Db 92 -----ValLeuGlyValAlaLeuSerAlaVal-ProCysMetLeuValLeu----- 106
    |||:::|||||
QY 221 AGCTGAATGCTCTTCTGTGCTTTGTGACAAACAAGACAGACAGATCCCAAGTCAA 280
    |||:::|||||
Db 107 -AlaLeuValAlaValAlaValLeuGlnArgProSerCysSerProArgProProPheSe 126
    |||:::|||||
QY 281 CAAGACCTATGCTGCTGGCCGCAAAACTGATTTGAGGTTGAATAAATGTTTATTT 340
    |||:::|||||
Db 126 rHis-----ValCysProAsnAlaTrpValGlnGlyPheGlnGlnLysCysTyrTyrPh 143
    |||:::|||||
QY 341 TTCTGAATACCAAGTAATGACATTCGCCAGGCGCTTGCATGGCACAGAGGCCCA 400
    |||:::|||||
```

```
Db 143 eSerAerPThrGlnLysSerAerTrpAsnSerSerArgGlnHisCysHisArgLeuGlyAlaSe 163
    |||:::|||||
QY 401 ACTAGCTCGGTTTGCACACACAGATGAGCTGAATTTCTTAATGAGATACAGGCGAATTT 460
    |||:::|||||
Db 163 rLeuAlaThrLeuAerThrLysGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 183
    |||:::|||||
QY 461 TGATTCCTGATTTGGCTTCACAGAGAGTGTGCAGAGCACCTTGGAAATGAGACAGACA 520
    |||:::|||||
Db 183 AspArgGTrpIleGlyLeuHisArgAlaGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 203
    |||:::|||||
QY 521 CACTGAGTATTAACAAC-----ACGATTCACATCCGCGGAGAGAAAGATTGGCTTACCT 574
    |||:::|||||
Db 203 ySerAlaPheThrAsnArgProValPheGlnLeuArgGlyGlyGlyArgCysAlaTyrLe 223
    |||:::|||||
QY 575 GAACAAACAACGGGATAGACAGTAACACAGATCTTATTCACCTGAGATGATGATGACAA 634
    |||:::|||||
Db 223 uAsnGlyAspGlyLysSerSerSerAlaLeuGlyHisSerGlnLysPheTrpValCysSerAr 243
    |||:::|||||
QY 635 GCTCAACAGCTAT 647
    |||:::|||||
Db 243 gAlaAspSerTyr 247
    |||:::|||||

RESULT 3
JH0822
Lymphocyte early activation antigen AIM/CD69 - human
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 09-Jul-2004
C:Accession: JH0822; I56167; S60753
R:Lopez-Cabreira, M.; Santis, A.G.; Fernandez-Ruiz, E.; Blacher, R.; Esch, F.; Sanchez-M
J. Exp. Med. 178, 537-547, 1993
A:Title: Molecular cloning, expression, and chromosomal localization of the human earli
militating receptors.
A:Reference number: JH0822; MIMD:93340630; PMID:8340758
A:Accession: JH0822
A:Molecule type: mRNA
A:Residues: 1-199 <ADP>
A:Cross-references: UNIPROT:Q07108; UNIPARC:UPI00000622D7; GB:222576; NID:G939938; PIDN
A:Note: the authors translated the codon CAA for residue 110 as Gln
R:Hamann, J.; Fiebig, H.; Strause, M.
J. Immunol. 150, 4920-4927, 1993
A:Title: Expression cloning of the early activation antigen CD69, a type II integral mem
A:Reference number: I56167; MIMD:93267093; PMID:8496594
A:Accession: I56167
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-199 <RBS>
A:Cross-references: UNIPARC:UPI00000622D7; GB:L07555; NID:G291897; PIDN:AA846359.1; PID
R:Santis, A.G.; Lopez-Cabreira, M.; Hamann, J.; Straus, M.; Sanchez-Madrid, F.
Eur. J. Immunol. 24, 1692-1697, 1994
A:Title: Structure of the gene coding for the human early lymphocyte activation antigen
ceptors.
A:Reference number: S60753; MIMD:94298875; PMID:8026529
A:Accession: S60753
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-199 <SAN>
A:Cross-references: UNIPARC:UPI00000622D7; EMBL:Z30426; NID:G525242; PIDN:CAA83017.1; P
C:Comment: This protein is the earliest inducible cell surface glycoprotein expressed in
C:Genetics:
A:Gene: GDB:CD69
A:Cross-references: GDB:132925; OMIM:107273
A:Map position: 12p13-12p12
C:Keywords: glycoprotein; phosphoprotein; receptor; transmembrane protein
F:33-64/Domain: transmembrane #status Predicted <TM>
F:85-194/Domain: C-type lectin homology <LCH>
F:18,30/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted
F:16/Binding site: carboxylate (Asn) (covalent) #status predicted

Alignment Scores:
Pred. No.: 4.05e-20 Length: 199
Score: 291.00 Matches: 62
```


GenCore version 5.1.8
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OM nucleic - protein search, using frame_plus_n2p model

Run on: May 23, 2006, 15:44:52 ; Search time 78.8 Seconds
(without alignments)
4247.089 Million cell updates/sec

Title: US-10-031-902A-36

Perfect score: 2160
Sequence: 1 gfgccctcgcgttccagf.....aataaaccacaatactactac 1206

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2849598 seqs, 92501592 residues
Total number of hits satisfying chosen parameters: 5699196

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODE=frame+n2p.model -DEV=xlp
-Q=/abs/ABSSWEB.spool/US10031902/runcat.23052006.145344.521/app.query.fasta.1
-DB=UniProt -QFMT=faetan -SUFFIX=n2p.rup -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pro -NOR=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abs02p
-USER=US10031902.@CGA.1.1.612.@runcat.23052006.145344.521 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : UniProt_7.2.1*
1: uniProt_sprot.*
2: uniProt_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1125	52.1	207	2	Q91V08 MOUSE
2	798	36.9	142	2	Q8V119 MOUSE
3	792.5	36.7	269	2	Q9D676 MOUSE
4	787	36.4	207	2	Q3UUY2 MOUSE
5	783	36.2	207	2	Q8BHH6 MOUSE
6	725	33.6	202	2	Q924B1 MOUSE
7	725	33.6	217	2	Q9WVF9 MOUSE
8	722	33.4	206	2	Q7TSP7 MOUSE
9	722	33.4	221	2	Q8BPR3 MOUSE
10	712	33.0	158	2	Q80Z35 MOUSE
11	672.5	31.1	196	2	Q8V121 MOUSE
12	650	30.1	156	2	Q7TSP6 MOUSE
13	592.5	27.4	233	2	Q925N7 RAT
14	586.5	27.2	235	2	Q5M911 RAT
15	561	26.0	204	2	Q80XD9 MOUSE
16	539	25.0	204	2	Q8V118 MOUSE

17	516	23.9	206	2	Q924B2 MOUSE	Q924B2 mus musculu
18	516	23.9	218	2	Q8C1T8 MOUSE	Q8C1T8 mus musculu
19	507.5	23.5	180	2	Q9DLS8_YBETA	Q9DLS8 murid herpe
20	376	17.4	191	2	Q9UHP7_HUMAN	Q9UHP7 homo sapien
21	345.5	16.0	133	2	Q6YID5_HUMAN	Q6YID5 homo sapien
22	304	14.1	188	2	Q6ZYD3_CHICK	Q6ZYD3 gallus galli
23	300.5	13.9	200	2	Q802S8_CHICK	Q802S8 gallus galli
24	296	13.7	188	2	Q6ZYD6_CHICK	Q6ZYD6 gallus galli
25	292	13.5	257	2	Q90636_CHICK	Q90636 gallus galli
26	291	13.5	199	1	CD69_HUMAN	CD69 homo sapien
27	291	13.5	199	2	Q53ZX0_HUMAN	Q53ZX0 homo sapien
28	290.5	13.4	173	2	Q9HD37_HUMAN	Q9HD37 homo sapien
29	285.5	13.2	154	2	Q8MUP7_HUMAN	Q8MUP7 homo sapien
30	282	13.1	149	1	CLC2B_HUMAN	CLC2B_HUMAN
31	279	12.9	85	2	Q5RF47_PONPY	Q5RF47 sus scrofa
32	276.5	12.8	200	2	Q8SPX1_PIG	Q8SPX1 sus scrofa
33	274	12.7	52	2	Q8V120_MOUSE	Q8V120 mus musculu
34	268.5	12.4	156	2	Q76LK0_COTJA	Q76LK0 coturnix co
35	258.5	12.0	199	2	Q95MQ1_BOVIN	Q95MQ1 bos taurus
36	245.5	11.4	160	2	Q6UVW9_HUMAN	Q6UVW9 homo sapien
37	243	11.2	159	2	Q8SPX0_PIG	Q8SPX0 sus scrofa
38	242	11.2	199	2	Q5M851_RAT	Q5M851 rattus norv
39	230.5	10.7	141	2	Q6S008_ADEG1	Q6S008 avian adeno
40	228.5	10.6	163	1	V239_F0WVPV	V239_F0WVPV
41	223	10.3	199	1	CD69_MOUSE	CD69_MOUSE
42	223	10.3	199	2	Q3U6A8_MOUSE	Q3U6A8 m bone matr
43	221.5	10.3	132	2	Q8R4K5_RAT	Q8R4K5 rattus norv
44	207	9.6	223	2	Q497F5_MOUSE	Q497F5 mus musculu
45	203	9.4	223	2	Q925G5_MOUSE	Q925G5 mus musculu

ALIGNMENTS

RESULT 1
Q91V08 MOUSE
ID Q91V08 MOUSE PRELIMINARY; PRT; 207 AA.
AC Q91V08;
DT 01-DEC-2001, integrated into UniProtKB/TREMBL.
DT 01-DEC-2001, sequence version 1.
DT 07-FEB-2006, entry version 22.
DE C-lectin related CLRB (Osteoclast inhibitory lectin) (C-type lectin domain family 2, member d).
DE domain family 2, member d).
GN Name=Clec2d, Synonyms=Ocll;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6;
RX PubMed=14990792; DOI=10.1073/pnas.0308304101;
RA Carlsyle U.R., Jamieson A.M., Gasser S., Clingan C.S., Araese H., Raulic D.H.;
RT "Missing self-recognition of Ocll/Clr-b by inhibitory NKR-P1 natural killer cell receptors";
RL Proc. Natl. Acad. Sci. U.S.A. 101:3527-3532(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BALB/C; TISSUE=Spleen;
RX PubMed=14990792; DOI=10.1073/pnas.0308304101;
RA Zhou H., Kartsoyan V., Hu Y.S., Elliott J., Quinn J.M., McKinsty W.J., Gillespie M.T., Ng K.W.;
RT "A novel osteoclast-derived C-type lectin that inhibits osteoclast formation.";

RL J. Biol. Chem. 276:14916-14923(2001).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=129/Sv;
RX MEDLINE=22359051; PubMed=12374791; DOI=10.1074/jbc.M209059200;
RA Zhai H., Kartsoyan V., Quinn J.M.W., Ly C., Gange C., Elliott J.,
RA Ng K.W., Gillespie M.T.;
RT "osteoclast inhibitory lectin, a family of new osteoclast
inhibitors";
RL J. Biol. Chem. 277:48808-48815(2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=PCR rescued clones;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strusberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.W., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.U., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=PCR rescued clones;
RG NIH MGC Project;
RL Submitted (OCT-2005) to the EMBL/GenBank/DBJ databases.
CC -----
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
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CC -----
DR EMBL: AF350409; AAK70357.1; -; mRNA.
DR EMBL: AY320031; AAO16529.1; -; mRNA.
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DR HSSP: Q07108; 1FM5.
DR Ensemble: ENSMUSG0000030157; Mus musculus.
DR MGI: MGI:213589; Clec2d.
DR GO: GO:0009897; C:external side of plasma membrane; IDA.
DR GO: GO:0005887; C:integral to plasma membrane; TAS.
DR GO: GO:0046703; F:natural killer cell lectin-like receptor bl. . .; IDA.
DR GO: GO:0005515; F:protein binding; IPI.
DR GO: GO:0010666; P:cellular defense response (sensu Vertebrata); TAS.
DR GO: GO:0045671; P:negative regulation of osteoclast different. . .; IDA.
DR GO: GO:0042270; P:protection from natural killer cell mediate. . .; IDA.
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DR InterPro: IPR001304; Lectin_C.
DR Pfam: PF00059; Lectin_C.1.
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DR SMART: SM00034; CLECT.1.
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KW
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Pred. No.: 1125.00 Matches: 207
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Best Local Similarity: 100.0% Mismatches: 0
Query Match: 52.1% Indels: 0

DB: 2 Gaps: 0
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QY 120 GAAGCGGCAAAATTCCTCCAAAGAAAAGGCAAGGACCATCTCCCTGAGCTTGTCG 179
DB 21 GluValGlyLysIleLeuGlnGlyLysArgHisGlyThrIleSerProGlnSerCysAla 40
QY 180 AAGCTTTACTGCTACTATGAGTGCATCATGTGCTCTCATCTAGCTGTAATTCCTCTTCT 239
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DB 201 GlnThrProPheProSer 207
RESULT 2
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AC 08v119;
DT 01-MAR-2002, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2002, sequence version 1.
DT 07-FEB-2006, entry version 19.
DE C lectin-related protein B (Fragment).
GN Name=Ocl; Synonyms=Clec2d;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
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OX NCBI_Taxid=10090;
RN [1]
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RC STRAIN=C57BL/6J;
RA Ploegastel B.F.M., Yokoyama W.M.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
CC -----
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CC Distributed under the Creative Commons Attribution-NonDerivs License
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DR EMBL: AF320599; AAL37199.1; -; Genomic_DNA.
DR HSSP: Q07108; 1FM5.

GenCore version 5.1.8
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OM nucleic - protein search, using frame_plus_n2p model

Run on: May 23, 2006, 16:09:18 ; Search time 1.2 Seconds

(Without alignments)
644.040 Million cell updates/sec

Title: US-10-031-902A-36

Perfect score: 2160

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Searched: 21570 segs, 2136119 residues

Total number of hits satisfying chosen parameters: 43140

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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5	167	7.7	223	US-10-511-937-2414	Sequence 2414, App
6	159	7.4	201	US-10-196-749-108	Sequence 108, App
7	157.5	7.3	190	US-11-268-890-4	Sequence 4, Appl1
8	155.5	7.2	376	US-10-505-928-77	Sequence 77, Appl1
9	151.5	7.0	231	US-10-511-937-2491	Sequence 2491, Ap

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12	129	6.0	188	7	US-11-268-890-2	Sequence 2, Appl1
13	126.5	5.9	1722	6	US-10-505-928-780	Sequence 780, Appl1
14	125	5.8	280	6	US-10-196-749-594	Sequence 594, App
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23	79	3.7	382	6	US-10-196-749-20	Sequence 20, Appl1
24	77	3.6	474	7	US-11-249-111-104	Sequence 104, App
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41	70	3.2	678	6	US-10-322-836-46	Sequence 46, App
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43	69.5	3.2	441	6	US-10-511-937-2427	Sequence 2427, App
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ALIGNMENTS

RESULT 1
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Sequence 2941, Application US/10511937
Publication No. US2006008836A1
GENERAL INFORMATION:
APPLICANT: EXPRESSION DIAGNOSTICS, INC.
APPLICANT: Wohlgemuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
APPLICANT: Ly, Ngoc
APPLICANT: Prentice, James
APPLICANT: Morris, MacDonald
APPLICANT: Rosenberg, Steven
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
FILE REFERENCE: 50661200104
CURRENT APPLICATION NUMBER: US/10/511,937
CURRENT FILING DATE: 2004-10-19
PRIOR APPLICATION NUMBER: PCT/US2003/012946
PRIOR FILING DATE: 2003-04-24
PRIOR APPLICATION NUMBER: US 10/131,931
PRIOR FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: US 10/325,899
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 3117
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2941
LENGTH: 191
TYPE: PRT
ORGANISM: Homo sapiens
US-10-511-937-2941
Alignment Scores:

GenCore version 5.1.8
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OM nucleic - protein search, using frame_plus.n2p model

Run on: May 23, 2006, 16:05:43 ; Search time 10 Seconds

(without alignments)
3166.858 Million cell updates/sec

Title: US-10-031-902A-36

Perfect score: 2160

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Scoring table:

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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RESULT 2
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; Sequence 10300, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 10300
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10300

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[illegible]

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/ TITLE OF INVENTION: DNA MOLECULES ENCODING HUMAN CLAX PROTEINS AND THEIR SO
/ TITLE OF INVENTION: PROTEINS
/ FILE REFERENCE: DB20 NP
/ CURRENT APPLICATION NUMBER: US/09/531, 056A
/ CURRENT FILING DATE: 2000-03-20
/ NUMBER OF SEQ ID NOS: 24
/ SOFTWARE: Patencin version 3.0
/ SEQ ID NO 13
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/ TYPE: PRT
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US-09-531-056A-13

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[illegible]

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; Sequence 13 Alignment US/09531056A
; Patent No. 6455683
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; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: DNA MOLECULES ENCODING HUMAN CLAX PROTEINS AND THEIR SO
; TITLE OF INVENTION: PROTEINS
; FILE REFERENCE: DB20 NP
; CURRENT APPLICATION NUMBER: US/09/531, 056A
; CURRENT FILING DATE: 2000-03-20
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 13
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-531-056A-13

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US-10-031-902A-36 (1-1206) x US-09-531-056A-13 (1-328)

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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - protein search, using frame_plus.n2p model

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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23	291	13.5	199	4	US-10-179-528-3	Sequence 3, App1
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42	217	10.0	100	4	US-10-176-558-578	Sequence 578, App
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45	217	10.0	100	4	US-10-176-483-578	Sequence 578, App

ALIGNMENTS

RESULT 1
US-10-379-127-24
; Sequence 24, Application US/10379127
; Publication No. US20040005592A1
; GENERAL INFORMATION:
; APPLICANT: Emclac, Peter C.R.
; APPLICANT: Dymac, Radoje
; APPLICANT: Goodrich, Ryle
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: MATERIALS AND METHODS RELATING TO THERAPY AND DIAGNOSIS USING TP
; FILE REFERENCE: NUVO-01CIP
; CURRENT APPLICATION NUMBER: US/10/379,127
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 09/799,451
; PRIOR FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 207
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-379-127-24

ALIGNMENT Scores:

Pred. No.: 3.43e-110
Score: 1125.00
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 52.1%
DB: 4
Length: 207
Matches: 207
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

US-10-031-902A-36 (1-1206) x US-10-379-127-24 (1-207)

QY 60 ATGTGTGTCAAGAGCTTCCCTACTATGCTTATGCCACAGCAGCCGCGAGAGTA 119

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Db 1 MetCysValThrLysAlaSerLeuProMetLeuSerProThiGlySerProGlnGluVal 20
QY 120 GAAGTGGTAAATTTCTCCAGAGAAAAGGACGGAACCATCTCCCTGAGTCTTGCT 179
Db 21 GluValGlyLysIleLeuGlnGlyLysArgHisGlyThrIleSerProGlnSerCysAla 40
QY 180 AAGCTTCTGCTCATGTAGAGATGCATGATCCCTCAGCTGATGCTGTAATGGCTCTTCT 239
Db 41 LysLeuIyrCysIyrTygIyValIleMetValLeuThrValAlaValIleAlaLeuSer 60
QY 240 GTTGGCTTGTCCAGCAACAAAGACAGAACAGATCCAGTCCAGCAACAGACTATGCTGCTTC 299
Db 61 ValAlaLeuSerAlaThrLysThrGluGlnIleProValAsnLysThrIyrAlaAlaCys 80
QY 300 CCGCAAACTGATGTGAGTGTGAAAATTAATGTTTTATTTTCTGAATACCAAGTAAC 359
Db 81 ProGlnAsnTrpIleGlyValGluAsnLysCysPheIyrPheSerGluIyrProSerAsn 100
QY 360 TGGACATTCGCCAGGCTTCTGCATGGACAGAGAGCCCACTAGCTGGTTTGACAC 419
Db 101 TrpThrPheAlaGlnAlaPheCysMetAlaGlnGluAlaGlnLeuAlaArgPheAspAsn 120
QY 420 CAGGATGAGCTGAATTTCTTAATGAGATACAAAGCGCAATTTGATTCCTGATTTGGCTTG 479
Db 121 GlnAspGluLeuAsnPheLeuMetArgIyrLysAlaAsnPheAspSerTrpIleGlyLeu 140
QY 480 CACAGAGAGTCTGCAGAGACACCTTGGAAGTGCAGACAGACACTGATGTAACAACAG 539
Db 141 HisArgGluSerSerGluHisProIyrTrpIyrThrAspAsnThrGluIyrAsnAsnThr 160
QY 540 ATTCCCATCCGGGAGAGAGAAAGATTGGCTACTCTGAACAACAAGCGGATCAGCAGTACC 599
Db 161 IleProIleArgGlyGlnGluArgPheAlaIyrLeuAsnAsnAsnGlyIleSerSerThr 180
QY 600 AGGATCTATTCACCTTCGATGTGATCTGTAGCAAGCTCAACAGCTATAGCTTCCACTGC 659
Db 181 ArgIleIyrSerIleuArgMetTrpIleCysSerLysLeuAsnSerIyrSerIleuHisCys 200
QY 660 CAAACTCTCTTTTCTCTCTCC 680
Db 201 GlnThrProPhePheProSer 207

RESULT 2
US-10-388-838-13
; Sequence 13, Application US/10388838
; Publication No. US20040180344A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Therapeutic Targets in Cancer
; FILE REFERENCE: 529452001600
; CURRENT APPLICATION NUMBER: US/10/388, 838
; CURRENT FILING DATE: 2003-03-14
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-388-838-13

Alignment Scores:
Pred. No.: 6.55e-79 Length: 277
Score: 831.50 Matches: 168
Percent Similarity: 66.2% Conservative: 16
Best Local Similarity: 60.4% Mismatches: 27
Query Match: 38.5% Indels: 67
DB: 4 Gaps: 3
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US-10-031-902a-36 (1-1206) x US-10-388-838-13 (1-277)

QY 24 AATCTGTAGTGAAGAACTGAGCTCCAGCTGTGAGATGTGTGTCAACAAAGCTTCCCTTA 83

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Db 1 AsnProIleValValThrGlnLeuLeuSerSerGluMetAsnIleThrArgAlaSerLeu 20
QY 84 CCTATGCTTATGCTCCACAGGACGCGC----- 107
Db 21 PrometLeuSerThrThrCysSerCysArgArgGluLysTrpAsnPheLeuGlyArgIyr 40
QY 107 ----- 107
Db 41 GluGlyThrPheAspTrpTrpIleGlyLeuHisArgAlaSerSerLysHisProTrpMet 60
QY 107 ----- 107
Db 61 TrpThrAspAsnThrGluIyrTrAsnAsnMetPheValTyrHisMetAsnAlaGlnCysLeu 80
QY 108 -----GTGAACTGGGTAAATTT 134
Db 81 LysLysProGlnGluGlyGlyLysSerProGlnIyrGlyValGlnCysIyrLysIle 100
QY 135 CTCCAAGGAAAAAGGACGGAACCATCTCCCTGAGTCTTGCTGTAAGCTTACTGCTAC 194
Db 101 LeuGlnArgLysSerIleuArgAlaIleSerProGlnSerSerAlaLysLeuIyrCysCys 120
QY 195 TATGAGTGCATGAGTCTCTCACTGAGCTGTAATGCTCTTCTGCTGCTTGTGCAGCA 254
Db 121 TyrGlyValIleMetValLeuThrValAlaValSerValSerVal----- 136
QY 255 ACAAAAGACAGACAGATCCCACTCAACAGACCTATGCTGCTTCCCGGCAAAATGGATT 314
Db 137 ThrLysThrGluGlnIleLeuIleAsnLysThrIyrAlaAlaCysProLysAsnTrpIle 156
QY 315 GGAGTGAATAATTAATGTTTATTTATTTTCTGAATACCAAGTAACCTGAGCATTCGCCAG 374
Db 157 GlyValGlyAsnLysCysPheIyrPheSerGluIyrThrSerAsnTrpThrPheAlaGln 176
QY 375 GCCTTTCGATGGACAGAGGCGCCAACTAGCTCGGTTTGACAAACGAGATGCTGAAT 434
Db 177 ThrPheCysMetAlaGlnGlnAlaGlnLeuAlaArgPheAspAsnGluLysGluLeuAsn 196
QY 435 TTCCTAATGATGATCAAGGCGAATTTTGATTTCTTGATTTGGCTGACAGAGTGTGTA 494
Db 197 PheLeuMetArgIyrLysAlaAsnPheAspSerTrpIleGlyLeuHisArgGluSerSer 216
QY 495 GAGCACCTTGGAGAGTGAACAGACACACTGAGTATATACACAGATTCCTATCCGAGGA 554
Db 217 GluHisProIyrTrpIyrThrAspAsnThrGluIyrAsnAsnMetIleProIleGlnGly 236
QY 555 GAGGAAAGATTTGCTTACCTGAACAAACGAGATCAGCAGATCTATTCGACTT 614
Db 237 ValGluThrCysAlaIyrIleuSerGlyAsnGlyIleSerSerSerArgHisIyrIlePro 256
QY 615 CGGATGTGATCTGTGCAAGCTCAACAGCTATAGCTTCCACTGCCAACTCCT 668
Db 257 ArgIleTrpIleCysSerLysLeuAsnAsnTyrSerIleuHisCysAspThrPro 274
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RESULT 3
US-10-335-009-2
; Sequence 2, Application US/10335009
; Publication No. US20040001804A1
; GENERAL INFORMATION:
; APPLICANT: Poruneelloor, Mathew A.
; APPLICANT: Boles, Kent S.
; TITLE OF INVENTION: LIT USES THEREOF IN IMMUNE SYSTEM MODULATION
; FILE REFERENCE: 11707.02/469687-7
; CURRENT APPLICATION NUMBER: US/10/335, 009
; CURRENT FILING DATE: 2002-12-31
; PRIOR APPLICATION NUMBER: US 09/475, 365
; PRIOR FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 191
; TYPE: PRT
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